## STIC-Biotech/ChemLib

170010

From:

Walicka, Malgorzata

Sent:

Saturday, October 29, 2005 10:56 AM

To:

STIC-Biotech/ChemLib

Please search SEQ ID NO:1 and 16 in 09/774,954. Please use also pending data.

Thank you.

Malgorzata A. Walicka, Ph.D.
Patent Examiner
Art Unit 1652, Recombinant Enzymes
USPTO, Remsen Building, Room 2C76
400 Dulany St.
Alexandria, VA 22313
Mail Room 2C70
Tel. (571) 272-0944, fax (571) 273-0944

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
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Vendors and cost where applicable STN:

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AK124093 Homo sapi
AC094844 Rattus no
AC134371 Rattus no
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AL807380 Mouse DNA
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AR509393 Sequence
AJ781501 Drosophil
CQ590403 Sequence
                    Bos tauru
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tive 0; Mismatches
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1 (bases 1 to 1514)
Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: US 6770987-A 2 07-AUG-2001,
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/mol_type="unassigned DNA"
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Sequence 2 from patent US 6270987.
AR163451.1 GI:16234056
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AJ66670
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BR103180 O-fucosyl
BD103190 O-fucosyl
D80002 Homo sapien
AX780153 Sequence
AL832023 Homo sapi
AR163453 Sequence
BD103191 O-fucosyl
AR163452 Sequence
BD103199 O-fucosyl
AR163457 Sequence
BD103196 O-fucosyl
AR163457 Sequence
AZ77777 Sequence
AZ7777 Sequence
AZ7781500 Pan trogl
AZ34580 Bos tauru
AZ781503 Bos tauru
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J567917 Sus scrof
AJ781499 Rattus no
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         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG 300
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    .1514
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/cell_type="myeloblast"
/tissue_type="brain"
/clone_lib="plabluescriptII SK plus"
/note="This="plabluescriptII SK plus"
fragments sequence was obtained by subcloning of the |
fragments derived from two cDNA clones (1 - 1066 was
derived from pf00933 and 1067 - 5189 was derived from
ha02567).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Hommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

To (bases 1 to 4560)

Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

Pobo,G., Han,M. and Wiemann,S.

Direct Submission

L. Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ)4510114; available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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Homo sapiens mRNA; cDNA DKFZp451J114 (from clone DKFZp451J114).
AL832023
                                                            CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
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Coganism="Homo sapiens"

/mol type="mkNA"

/db_xref="RzPD:DKFZg451J114"

/db_xref="RzPD:OFFZg451J114"

/db_xref="homo skeletal muscle"

/clone "DKFZg451J114"

/clone "Dis="homo skeletal muscle"

/clone "lib="451" (synonym: hlcc1). Vector pSport1; host

DH10B; sites Noc1 + Sal1"

/dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 CATGTGCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TITGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT
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Best Local Similarity 99.7%;
Matches 1510; Conservative C
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	ansferase.  GI:226487  d	Best Local Similarity 99.9%; Pred. No. 0;  Matches 1448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  Qy 66 GAACCAGGCCGATCTTGGGCTCTGGGATTTGCAAAGCTGCTAAACCGTACCTT 125
Query Match         95.6%; Score 1447.4; DB 6; Length 5009;           Best Local Similarity         99.9%; Pred. No. 0;           Matches 1448; Conservative         0; Mismatches         1; Indels         0; Gaps         0;           Qy         66 GAACCAGGCCGATCATTTTGGGATTTGCAAAGCTGCTAAACGTACTT         60           Db         1 GAACCAGGCCGATCATTTTTTTTTTTTTTTCCAAAGCTTTCTTT	486 GGAACATCCGGTGCTTGCCCTGCCAGGGCCCAGCCCAGTTCCCCGTCCTAGAAGACA	OY 1026 GGGGGGCTCCGGGGTCTCTTTTGGGCGTGGGAGGCCCCCTAACTGGG 1085

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                                                                                                                                                                                                                                                                                                                      ATGCCCGCGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC
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                                                                                                                                                                                                                                                                  6; Length 1300;
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    isov
    forganism='Unidentified'

                                                08/792498, 26-NOV-1997
                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                Score 1163.4; DB 6
Pred. No. 2.7e-284;
0; Mismatches 1;
                                                                                                                                 Location/Qualifiers
                                  17-DEC-1997 JP 1998532877
31-JAN-1997 US 08/792498,26
G WANG, MICHAEL W SPELLWAN
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
                                                                                                                                                                     Location/Qualifiers
1. 1300
/ organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
           JP 2001527389-A/2
25-DEC-2001
                                                                                                                                                                                                                                                                  76.8%;
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Best Local Similarity 99.9
Matches 1164; Conservative
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         GAAGGAAACCCCTTTGGCCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
                                                           CTTTTACAGGCATTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT
                                                                             CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT
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Wang, Y. and Spellman, M.W.
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Db 241 AGCTTGGAGGATTTCATGGAGCTGGCACCCCACCCACTGGCCCCCTGAGAAGCGGGTG 300  Qy 301 GCATACTGCTTTGAGGTGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAGG 360  Db 301 GCATACTGCTTTGAGGTGCCCAGCCAAGCCCAGATAAAAAAGACGTGCCCCATGAAG 360	361	Oy 421 CTITITACAGGCATTICCTTCAGTGCTTCCTACAGGAACAATGGAGCCAGAGATTITCT 480	Qy 481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGTTCCCGGTCCTAGAA 540	Qy         \$41         GAACACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGCATTCATCTGCGCATTGGCTCT 660	Oy 661 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGACTGCAGGCTCGCACTTCATGGCC 720	Qy 721 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCAGCGGCCCCCTCACGATGACTATGTGC 780	Oy 781 CTGCCTGACCTGAAGAGAGATCCAGAGGCTGTAAAGCTCTGGGTGAGGTCGCTGGATGCC 840	Ay 841 CAGTCGGTCTACTTGCTACTCGACAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900	OY 901 AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960	Oy 961 CTCGGCCAAGCCGACCATTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020	1021 CGGGAGCGGGACCTCCAGGGC 	Oy 1081 CTGCGGGGGTTCTGATT 1100  Db 1081 CTGCGGGACGATTCTGATT 1100	RESULT 13   BD103196
	AACAGCTCTTC                  AACAGCTCTTC	Qy     901     AAAGGGAAGGTGAAGGTGGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC     960       Db     1036     AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC     1095	Oy 961 CTGGCCAAGCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCTTTGTGAAG 1020	Oy 1021 CGGGACCTCCCAGGGACCCCTCTTTTTTTTCGGCATGGACAGGCCCCCTAAG 1080	Oy 1081 CTGCGGGACGACTTCTGATTCTGGCCGGAGCACCACCCTCTGATCCTGGAGGGACCAG 1140	Oy 1141 AGTCTGAGCTGCTTCCAGCCAG 1165  Db 1276 AGTCTGAGCTGCTTCCAGCCAG 1300	AR163457	ITION Sequence 16 from patent US 6270987. SION AR163457 ON AR163457.1 GI:16234062 RDS		AUTHORS Wang, Y. and Spellman, M.W. TITLE O-fucosyltransferase JOUNNAL Patent: US 6270987-A 16 07-AUG-2001;	Bource	Query Match Query Match Query Match Sest Local Similarity 100.0%; Pred. No. 3.4e-268; Length 1100; Matches 1100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy         1 ATGCCGGGGGTCCTGGACCGGGTTACTGCTCTACTGCCCTGCATGGGCGC 60	00   01   TTTGGGAACCAGGCCGATCACTTCTTGGCATTTGCAAAGCTGCTAAACCGT 120   11

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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                         CTGCCTGACCTGAAGGAGTCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGAAGCC
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Patent: JP 2001527389-A 9 25-DEC-2001;
GENENTECH INC
OS Unidentified
PN JP 2001527389-A/9
PD 25-DEC-2001
PF 17-DEC-1997 JP 1998532877
PR 31-DAC-1997 JP 1998532877
YANG WANG, MICHAEL W SPELLMAN
PC C12N15/54 C12N9/10, C07K16/40
CC Strandedness: Single;
CC Topology: Linear;
CC O-fucosyltransferase
FT Source 1. 1100
FT Source / Organism='Unidentif

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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                                                      Martinez-Duncker, I., Mollicone, R., Candeller, J.J., Breton, C. Oriol, R.
                                                                                                                                                                                                                                                                                                                                               Av. Paul
                                                                                                A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases: phylogeny and identification of conserved peptide motifs Glycobiology 13 (12), 1C-5C (2003)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan
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Submitted (06-JUL-2004) Oriol R., U504,
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
10.1167
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1.1167
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Fut12 gene; pofut1 gene; protein-O-fucosyltransferase 1. Pan troglodytes
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                                                               GCATACTGCTTTGAGGTGGCAGCCCAGCAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360
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  CATGIGICCIACCAGAAGIACTICAAGCIGGAGCCCCICCAGGCTIACCAICGGGICAIC 309
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8780412 Total number of hits satisfying chosen parameters: 4390206 seqs, 2959870667 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqn2004as:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* N Geneseq 16Dec04:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Add56824 Novel can Abl13947 Drosophil Abl13946 Drosophil Aaf23894 Human sec Abl13894 Drosophil Abl13952 Drosophil Abn44539 Human spl Aaz98210 Human spl Aav65632 Human hea Aav65633 Plasmid c Acn40746 Tumour-as Adf81754 Leukaemia Aal03344 Human rep Ach35532 Human end Ach32225 Human end Aak51510 Human p Aak52494 Human p Aav65634 First E Aad07629 Human s Aak79915 Human i Description SUMMARIES AAV65633 ACN40746 ADF81754 AAK51510 AAK52494 AAV65634 AAN07629 AAN79915 AAL033344 ACH35532 ACH32225 ADQ56824 ABL13952 ABN44539 AAZ98210 ABL13947 ABL13946 AAF23894 ABL13894 AAV65632 Query Match Length DB 5009 915 10331 10331 477 1209 3264 1545 3793 3567 1510.8 1460.2 1450.2 1447.4 854.8 608.6 608.6 441 406.2 166.4 150.4 123.2 108.6 71.8 60 Score No. Result

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υ	22	46.2	3.1	2000	œ	ADA71938	Ada71938 Rice gene
	23	42.4	2.8	1438	æ	ACA31561	Aca31561 Prokaryot
υ	24	41.2	2.7	114793	4	AAD08215	Aad08215 Human gen
O	25	40.6	2.7	558	Ŋ	AAH97782	Aah97782 Murine 7-
	56	40.6	2.7	2036	13	ADT44716	Adt44716 Bacterial
	27	40.4	2.7	5019	13	ADQ80232	Adq80232 Brain-spe
	28	40.4	2.7	5704	12	ADQ84111	Adq84111 Human tum
	59	40.4	2.7	5932	10	ADB75488	Adb75488 Prostate
	30	40	2.6	40	~	AAV65637	Aav65637 Primer am
	31	40	2.6	40	~	AAV65635	Aav65635 Northern
	32	40	5.6	1554	œ	ADA69815	Ada69815 Rice gene
	33	39	2.6	372	ω	ACA43606	Aca43606 Prokaryot
	34	39	5.6	1079	10	ADC37615	Adc37615 Human nuc
	35	39	5.6	1131	11	ABD01472	Abd01472 Pseudomon
	36	39	2.6	1209	٣	AAA61286	Aaa61286 Human sec
	37	39	5.6	1209	œ	ADA40219	Ada40219 Human sec
	38	39	5.6	1209	10	ADD37708	Add37708 Human sec
	39	39	5.6	1209	2	ADA56378	Ada56378 Gene enco
	40	39	5.6	1353	7	ABD01484	Abd01484 Pseudomon
	41	39	5.6	1404	10	ADC16737	Adc16737 Human mod
	42	39	5.6	1528	4	AAH15283	Aah15283 Human cDN
	43	39	5.6	1555	4	AAS44695	Aas44695 Human ful
	44	39	5.6	1566	4	AAS01567	Aas01567 Human sec
	45 ,	39	5.6	1575	9	ADI16595	Adil6595 Human NOV

## ALIGNMENTS

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O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                                                                        Location/Qualifiers
1. .1100
/*tal
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sequence is claimed for in claim 9"
1. .1098
/*tag= a
/product= "human heart O-fucosyltransferase
                                                                Human heart O-fucosyltransferase encoding DNA.
               AAV65632 standard; DNA; 1514 BP.
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                                                16-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                  misc_feature
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26-NOV-1997;
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                               AAV65632;
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RESULT 1
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        AAV65632
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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.

WPI; 1998-437477/37. P-PSDB; AAW80571.

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/note= "insert coding for human O-fucosyltransferase."
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781 CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
                        CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
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                                  This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (ESP) domain of a polygeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, ed. wutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of -fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EFG domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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100.0%; Score 1514; DB 2; Length 1514;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1514; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                 Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
                 Fig 12A; 90pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1512.4;
Pred. No. 0;
0; Mismatches
 /note= "polyhistidine tag'
                                                                                                                                                                                                                                               Example; Page 49-57; 90pp; English
                                                                                     97US-00792498
97US-00978741
                                                                 97WO-US023401
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.9%;
Matches 1513; Conservative
                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                             Spellman MW
                                                                                                                                                                  1998-437477/37.
                                                                                                                                                                                                                                                                                                                                                                                  fucosyltransferase
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                      WO9833924-A1
                                                                 17-DEC-1997;
                                                                                    31-JAN-1997;
26-NOV-1997;
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장염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide mammals. The invention also relates to nucleic acid and polypeptide in sequences at least 80% identical to the TAT nucleic acids and polypeptide, and nucleic acids and polypeptide, and nucleic and polypeptide, and methods and compositions for the treatment or cancer in mammals. TAT polypeptides, nucleic acids, and the polypeptide, is and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cancer, cancer, cancer, system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probbs, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                         Tumour-associated antigenic target (TAT) cDNA DNA326813, SEQ ID NO:5725.
                                                                                                                                 Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; call proliferative disorder; breast cancer; colorectal cancer; lung cancer; overian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; malanoma; leuksemia; hybridisation probe; chromosome identification; chromosome mapping; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 5725; 7273pp; English.
                          ACN40746 standard; cDNA; 5218
                                                                                                                                                                                                                                                                                                                            29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                     02-OCT-2002; 2002US-0414971P.
                                                                                18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y;
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Matches 1512; Conservative
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P-PSDB; ABM82223.
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                                                                                                                                                                                                                                               Homo sapiens.
                                                     ACN40746;
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                                                 GCATACTGCTTTGAGGTGGCAGCCCAGGAGACCCCAGATAAGAAGACGTGCCCCATGAAG
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  of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, for the preparation of a medicament for treating leukaemia.
                                                                                      Sequence 5266 BP; 1280 A; 1278 C; 1331 G; 1346 T; 0 U; 31 Other;
                                                                                                                             DB 10; Length 5266;
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                                                                                                                                                                      3; Indels
                                                                                                                          Score 1509.8;
Pred. No. 0;
0; Mismatches
                                                                                                                          99.7%;
                                                                                                                                              Best Local Similarity 99.8
Matches 1511; Conservative
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                                                                                                                                                               TCCATATCCCAGGGCATAGGACTTGCAGGTTCCTAGGAGCAGGAGCATCTCCCATCGCAC
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(SCHO/) SCHOCH C.
(KERN/) KERN W.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to production of other cytokines in other cell proliferation or call differentiation or which may induce production of other cytokines in other cell populations. The polymeloetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity is and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SQD ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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   Y;
Wang ZW;
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Best Local Similarity 96.4%; Score 1460.2; DB 4; Length 5230;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 1462; Conservative 0; Mismatches 3; Indels 0;
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   Xu C, Cao
Chen R,
Asundi V, Zhou P, X
J, Zhang J, Ren F,
Goodrich R;
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Drmanac RT, P
Wang D, Wang J
Wejhrman T, G
                                                                                                                   WPI; 2001-476283/51.
P-PSDB; AAM78377.
Liu C,
hao QA, W
Yang Y,
Tang YT, Liu
Ma Y, Zhao Q
Xue AJ, Yang
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomedulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

WPI; 2001-476283/51. P-PSDB; AAM79361.

Claim 1; Page 4424-4425; 6221pp; English.

ZW;

Cao Y; R, Wang

chen

Drmanac RT, Asundi V, Zhou P, Xi Wang D, Wang J, Zhang J, Ren F, Wejhrman T, Goodrich R;

Liu C, nao QA, W Yang Y,

Zhao

Tang YT, Ma Y, Zh Xue AJ,

(HYSE-) HYSEQ INC

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. 20-JUN-2000; 2000US-00598075. 19-JUL-2000; 2000US-00620325. 01-SEP-2000; 2000US-00654936. 15-SEP-2000; 200US-00653561. 20-OCT-2000; 2000US-0069325. 30-NOV-2000; 2000US-0059325.

2001WO-US004098

05-FEB-2001;

09-AUG-2001

WO200157190-A2

Homo sapiens.

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concided polypeptides (AAAN'832)-AAAN80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem call growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, infulbin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEO ID NO 2110 (AAKS2881), 2111 (AAKS2882) and 3666 (AAMN80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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invention relates to polynucleotides (AAK51456-AAK53435) and
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                                                                                                                                                                                                                                                                                                                               Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                             4; Length 4850;
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Pred. No. 0;
0; Mismatches
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Best Local Similarity
Matches 1459; Conserv
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Human polynucleotide SEQ ID NO 2023

(first entry)

06-NOV-2001

AAK52494

AAK52494
ID AAKE
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AC AAKE
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DT 06-1
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AAK52494 standard; cDNA; 4850

RESULT 6

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This represents a first ECOR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial CDNA encodes for a protein of unknown function from wyeblast cel line KG-1. The invention provides a human heart of ucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 GGCTGTCCTTCGTTGGATTGGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCATGT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
1526 CTCCGTCTTCTGGTCCACTCTGCTCTGAGCAGCCTGGGATGCTGAACTCTTCAGAGAAT
                                                                                                                                                                                                                                             O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.6%; Score 1447.4; DB 2; Length 5009; Best Local Similarity 99.9%; Pred. No. 0; Matches 1448; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                         First EcoR1 nucleotide fragment of human KIAA0180.
                                                                    1490 GTGGTTTTTGAAATCATTGAATTC 1514
                                                                                   GTGGTTTTTGAAATCATTGAATTC 1670
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                                                                                                                                                       AAV65634 standard; cDNA; 5009
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overexpression of the enzyme.
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                                                                                                                                                                                                   (first entry)
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P-PSDB; AAW80577.
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26-NOV-1997;
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                                                        GCCCCATGAAGGAAACCCCTTTGGCCCATTCTGGATCAGTTTCATGTAGAGTTTCA
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                                                                                                                                                                       TTCTATAATTTTGATACAAGGTCATGACTATCCTAGAACTCTCTGTGGTTTTTGAAAATC
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                              ACTCTGCTCTGAGCAGCCTGGGATGCTGAACTCTTCAGAGAGATTTTTTATAGAGAGAT
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                ATCCCAGGGCATAGGACTTGCAGGTTCCTAGGAGCAGGAGCATCTCCCATCGCACGTGCT
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/transl_except= (pos:442. .444, aa:Xaa)
/note= "Xaa equals any of the naturally occu
acids; CDS does not include start codon"
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                                     GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTGGCATA
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                                                                                                                                                                                                     AAD07571-AAD07645 represent cDDNAs corresponding to 25 human secreted protein genes, and AAE33052-AAE33126 represent the protein they encode. AAE03127-AAE03150 represent human secreted proteins tragments. The genes can their corresponding secreted proteins are useful for preventing. The genes can their corresponding secreted proteins are useful for preventing. treating or amelicating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the mutations in the new genes. Specific uses are described for each of the corresponding products for the diagnosis or treatment of mutations in the new genes. Specific uses are described for each of the proprietative disorders, cancer, tumours, focetal and developmental corrective disorders, diseases of the immune system, and include developing products for the diagnosis or treatment of proliferative disorders (e.g., Alzheimer's disease, Parkinson's allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders (e.g., Alzheimer's disease, pathorogical disorders (elg., Alzheimer's disease, angiogenic disorders, diabetes, atheroscilerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and corrections. The proteins can also be used to aid wound healing and niceptions. The proteins can also be used to aid wound healing and or preservative to modify storage properties. Antiding partners, and in chemotaxis, and can be used to subporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic symptoms associated with the disorders mentioned above, and in diagnostic immunosassy e.g., radioimmunosassy or enzyme linked immunoscopent assay (ELISA). The present sequence represents a human secreted protein.
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                                                                                          Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 34727; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially

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cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietid antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                        1072 CCCCTAAGCTGCGGACGACTCTGATTCTGGCCGGAGCACCAGACCCTCTGATCCTGG
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                                                                                            Match 40.2%; Score 608.6; DB 4; Length Local Similarity 98.6%; Pred. No. 4e-166; es 614; Conservative 0; Mismatches 9; Indels
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             system antigen is condition.
                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                      6127 CTGTGCTTCTTCCTGCAGGTGAAGGTGGTGAGCCTGAAGCTTGAGGTGGCCCAGGTCGAC
                                                                                                                                                                                                                                                                                                                              CTGTACATCCTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTTCACTGCC
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                                                                                                                                                                  Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
                                                                                                                                                                                              40.2%; Score 608.6; DB 4; Length 10331; 98.6%; Pred. No. 4e-166; ive 0; Mismatches 9; Indels 0;
                                                   Disclosure; SEQ ID NO 6032; 1297pp + Sequence Listing; English.
             Isolated nucleic acid molecule encoding a reproductive used in preventing, treating or ameliorating a medical
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Best Local Similarity 98.6
Matches 614; Conservative
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Mybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed sequence data cot this patent did not form part of the printed sequence data cot this actionic format directly from USPTO at sequence that was sequence. The sequence that sequence cot sequence of the sequence that the sequence cot sequence and sequence that the sequence cot sequence contained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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Human; 88; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 22744; 44pp; English.
                                                                                                                                                                                              30-JUL-2001; 2001US-00918995.
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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                                                                                                                                                                                                                                                                                  (DRMA/) DRMANAC R T.
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                                                                                                          US2003073623-A1.
                                                                Homo sapiens
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for dentifying expressed general mapping of the human genome, in forensics, in assessing biodiversities, or in indentifying mutations. The forensics are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from USPTO at sequence. The sequence contained in electronic format directly from USPTO at Sequence.
                                                                310 CTTCCAGCCAGCCTGCCAGCCAGAGGTGCTCCGGGATTGCAAACTCCTCTTCTCACCTG 369
                                                                                   370 CCAAAGATGGAGAAGAGTGCCAGGGACCCTCAAGGAGGAGACGCTCCATATCCCAGGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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                                                                                                                                  Dickson MC,
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                                                                                                                                                                                                                                                                                                                                                          Human endothelial cell cDNA #358.
                                                                                                                                                                                                                                                         ACH32225 standard; cDNA; 479 BP.
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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Sequence 479 BP; 99 A; 140 C; 143 G; 97 T; 0 U; 0 Other;

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250 CTGATTCTGGCCGGAGCACCAGACCTCTGATCCTGGAGGGACCAGAGTCTGAGCTGGTC

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or
                                                                                                                                                                                                                        928 AAGCCTGAGGCCCCAGGTCGACCTGTACATCCTCGCCCAAGCCGACCACTTTATTGC
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                                                                                                                                                                31 GAGAGITAIGIGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAGGTGGTGAGCCTG
                                                                                                                                                                                                                                                                                 91 AAGCCIGAGGIGGCCCAGGICGACCIGIACAICCICGGCCAAGCCGACCACTITAITIGGC
                                                                                                                                                                                                                                                                                                                                                                                                    151 AACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGGACCTCCAGGGGAGGCCG
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         canine microarray; drug screening; toxicity assay;
environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
                                                           ;
0
     Length 479;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel canine microarray-related DNA sequence SeqID8126.
  Score 441; DB 9; L
Pred. No. 6.9e-118;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2002; 2002US-0377240P.
  29.1%;
ilarity 98.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porter M,
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                             Similarity
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                                                  444;
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Matches
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1 CACCAATCTCCATGTGTNCTACCAGAAGTACTTCAAGCTNNAGCCCCTCNAGGNNTACCA

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GAGATTTTCTCCAAAGGAACATCCAGTGCTGGCCC-CCCGGGAGCCCCCGCCCAGTTCCC

GAGATTTTCTCCCAAAGGAACATCCGGTGCTTGCCCTGCCAGGCCCCAGCCCCAGTTCCC

CGTCCTAGAAGAACACACGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAA 591 GACGGGAGAGGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCG 420 GACGGGAGAGGCCCACATTCTCACCCACCTCATCCGGCCGTACGTGGGCATTCACCTGCG

CATTGGCTCTGACTGGAAGAA 671

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This invention is related to a novel isolated canine mucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine mucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention may be useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that conducing electronic Northerns that allow the user to determine the cell producing electronic Northerns that allow the user to determine the cell or type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The similarity of a toxic response to one or more individual compounds. The cethologies such as those of the liver (liver necrosis, fatty liver of the toxins. The methods are also useful for predicting or elucidating confiscating due to the similarity of the expression profile compound or test agent will induce various specific of the potential cellular pathways influenced, induced or modulated by the compound or test agent when toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the product or a canine microarsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 610 BP; 155 A; 171 C; 149 G; 129 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of a canine microarray of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 406.2; DB 1:
Pred. No. 1.1e-107
0; Mismatches 54
                                                      SEQ ID NO 8126; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.8%;
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Matches 446; Conservative
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   TGGAGAAGCTGGCACCCACTGGCCCCCTGAGAAGCGGGTGGCATACTGCTTTGAGG
                                                                                                                                                                                               374 AACGATATAGCCTTCAGCAGGAGAAGAACGATCCAGACAAGCCCAATTGCCACGCCAAGG
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                                                               314 TGTGGCACCTGGCCGACGACATTTGGCCAGAATCGGAGCGAGTGTCATTTTGCTACAAGG
                                                                                                                                   -----TGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAGG
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pharmaceutical; gene; ss.
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ABL13946/c
ID ABL13946 standard; cDNA; 3264
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                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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Sequence 9
Sequence 7
Sequence 8
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Sequence 4
Sequence 1
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-978-741-5

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seq length: 200000000
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14477.4
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Perfect score:
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Sequence 2,

28 37.6 29 37.4 29 37.4 31 37.4 31 37.4 32 37.7 33 37.2 34 3 37.2 35 37.2 36 37.2 37 37 37.2 37 37 37 37.2 37	1, Appli 1, Appli 1, Appli 11943, A 12011, A 12011, A 13025, A 1, Appli 1, Appli		Gaps 0; 39GCGC 60 
28 37.6 29 37.4 29 37.4 31 37.4 31 37.4 32 37.7 33 37.2 34 3 37.2 35 37.2 36 37.2 37 37 37.2 37 37 37 37.2 37	\ N \text{N \tex		Length 1514; Indels 0; CTGCCCCTGCATG
SOURCE CONTRACTOR CONT	28 37.8 2.5 4411529 29 37.4 2.5 18637 31 37.4 2.5 18633 32 37.2 2.5 77536 35 37.2 2.5 1218 36 37.2 2.5 10265 37 37.2 2.5 10265 38 37.2 2.5 10265 39 37 2.4 5962 39 37 2.4 5975 41 37 2.4 5975 43 36.8 2.4 3591	ALIGNMENTE SGUT 1  -08-978-741-1 Sequence 1, Application US/08978741 Sequence 1, Application US/08978741 Sequence 1, Application US/08978741 Sequence 1, Application US/08978741  TILE OF INFORMATION: OF ECONOMICE ADDRESS: ADDRESSES: ADRESSES: ADDRESSES:	TOPOLOGY: Linear  -08-978-741-1  Query Match  Best Local Similarity 100.0%; Score 1514; DB 3; Length 1514;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1514; Conservative 0; Mismatches 0; Indels 0; Gaps
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	RESULT 2 US-09-333-729A-2 is Sequence 2, Application US/09333729A is Bedrent No. 627087 is GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Wang Yang APPLICANT: Wang Yang TITLE OF INVENTION: O'PLOCSFYLTARSFERSE CURRENT APPLICATION NUMBER: US/09/33, 729A CURRENT FILING DATE: 1999-06-15 is CURRENT FILING DATE: 1997-11-26 is PRIOR FILING DATE: 1997-11-26 is DATE OF SEQ ID NOS: 21 is DATE OF SEQ ID NOS: 21 is TYPE: DNA is ORGANISM: Homo Sapien US-09-333-729A-2	Ouery Match Best Local Similarity 100.0%; Score 1514; DB 3; Length 1514; Best Local Similarity 100.0%; Pred. No. 0; Matches 1514; Conservative 0; Mismatches 0; Indels 0; Gy 1 ATGCCCGCGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGGCG 60 Db 1 ATGCCGGGGGCTCCTGGGACCCGGCCGGTTACTGCTCTACTGCCCCTGCATGGGGGCG 60		181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC
61 TTTGGGAACCAGGCCGATCACTTCTTGGCCTCTGGCATTTGCAAAGCTGCTAAACCGT 120 61 TTTGGGAACCAGGCCGATCACTTCTTGGCCTCTTGGCATTTGCAAAGCTGCTAAACCGT 120 121 ACCTTGGCTGCTCTCTTGGATTGAGTACCAGCATTTGCAAAGCTGCTAAACCGT 120 121 ACCTTGGCTGTCCTCCTTGGATTGAGTACCAGCATCACAGCCTCTTCACCAACCTC 180 121 ACCTTGGCTGTCCTCCTTGGATTGAGTACCAGCATCACAGGCTTCCACACACCTC 180 121 ACCTTGGCTGTCCTCCTTGGATTGAGTACCAGCACTCACAGGCTTCCACACACCTC 180 181 CATGTGTCTCCTACCAGAAGTTCATGAGTACAGGCTCCTCTTCACCACAGGCTCATC 240 181 CATGTGTCTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC 240 181 CATGTGTCTTCACAGAAGTACTTCAAGCTGGAGCCCCTCCAGGAGCTACCATCGGGTCATC 240 181 CATGTGTCTTCATGGAGAAGTTCATGGAGCCCCCTCAGGAGCGGTCATC 240 182 AGCTTGGAGATTTCATGGAGAAGCTGGCCCCCACAGGCCTTACCATCGGGTCATC 300 183 AGCTTGGAGAAGTTCATGGAGAAGCTGGCCCCCTGAGAAGCGGGTG 300 184 AGCTTGGAGAAGCTGGCAGCCCAGCCCAGATAAGAAGACGTGCCCCATGAAG 360 185 AGGAAACCCCTTTGGCCCATTCTGGGATCAGTTAAAGAAGACGTGCCCCATGAAG 360 186 AAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAGTCGGAG 420 186 AAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAGGTGGGAG 420 187 AAAGGAAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGATTTCAACAGTCGGAG 420 188 AAAGGAAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGATTTTCATTAACAGGAATTTTTTTAACAGGAATTTTTTTT	481 CCAAAGGAACATCCGGTGCTGCCAGGAGCCCCAGCTCCCTAGAA 540  [	181   CTGCCTGAACCTGAAGGAATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840	901 AAAGGAAAGGTGAAGCTGAAGCCTGAAGCCTGAGGTGGCCCAGGTCGACTGTACATC 960	CCCCTAAG CCCCTAAG CCCCTAAG AGGGACCAG HIHHHA AGGGACCAG

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241 AGCITGGAGGAITTCATGGAGAAGCTGGCCCCCCCCCCTGAGAAGCGGGTG 300 4476 ACCITGGAGGAITTCATGGAGAAGCTGGCCCCCCCCCCCC	481   COMMAGGAACATCCGGTCCTTGCCCTCGCAGCCCAGCCCAGTTCCCCTCTCAGA   4715   COMMAGGAACATCCGTTCCCTTCCCTCCGCCCCAGCCCCAGCCCCAGTTCCCCTCTCAGAGAACATCCTCCTCCTCTCAGAGACACCCCCTCAGAGAACACCCCCTCAGAGAACACCCCCTCAGAGAACACCCCCTCAGAGAACACCCCCTCAGACACACCCCCTCAGAGAACACCCCCTCACCCCTCTCAGACACACCCCCTCACCCCTCTCCCCCTCTCTCCCCCCTCTCTCTCCCCCC

Oy 1326 TTCTGCTCTTCTGGGAATTTCTCACACTGGCAAAGCAGCTCCGTCTTCTGGTCC 1385	RESULT 5 US-09-333-729A-8  i Sequence 8, Application US/09333729A  i Patent No. 6270987  i GENERAL INFORMATION:  i APPLICANT: Wang Yang  i TITLE OF INVENTION: O-Fucosyltransferase  i TITLE REFERENCE: P10412101-Substitute  CURRENT APPLICATION NUMBER: US/09/333,729A  CURRENT APPLICATION NUMBER: US/09/333,729A  i PRIOR APPLICATION NUMBER: US 08/798,741  PRIOR APPLICATION NUMBER: US 08/798,741  i NUMBER OF SEQ ID NOS: 21  i SEQ ID NO 8  i LENGTH: 5009  i TYPE: DNA  c ORGANISM: Homo Sapien	Query Match         95.6%; Score 1447.4; DB 3; Length 5009;           Best Local Similarity         99.9%; Pred. No. 0;           Matches 1448; Conservative         0; Mismatches         1; Indels         0; Gaps           Qy         66 GAACCAGGCCGATCACTTTTGGCATTTGCAAAGCTGCTAAACCGTACCTT         125	186 GTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATCAGCTTT	0y         306         CTGCTTTGAGGTGGCAGCCAAGCCCAATAAGAAGACGTGCCCCATGAAGAAGG         365           1
246 GGAGGATTTCATGGAGAAGCTGGCCCCACTGGCCCCCTGAGAAGCGGGTGGCATA 305				1081 GGACGAGTTCTGGCCCGGAGCACTCTGATCCTGGAGGACCCAGAGTT 1145 1021 GGACGAGTTCTGGCCCGGAGCACCCTTGATCCTGGAGGGACCAGAGTT 1145 1021 GGACGAGTTCTGGCCGGCGCGCGAGCCTCTGATCTGGAGGGACCAGAGTTT 1080 1146 GGACGGTTCTTCCAGCCGGGCCTGGCAGCCTCTGGATTGCAAACTCCTT 1080 1081 GAGCTGGTCCTTCCAGCCAGGCCTGGCAGCGTGCTCCGGGATTGCAAACTCCTT 1205 1081 GAGCTGGTCCTTCCAGCCAGGCCTGGCAGGGGATTGCAAACTCCTCT 1205 11081 GAGCTGGTCCTTCCAGCCAGGAGAGGCCCCTCAAGGAGGGATTGCAACTCCTT 1205 11081 GACCCACGCCAAAGATGGAGAAGAGTGCCAGGGATTGCCAAAGAACGCTCCAT 1205 11081 GACCCAGCGAAAGATGGAGAAGAGTGCCAGGGAACCCCTCAAGGAGGAGACCCTCCAT 1205 11081 GACCCAGGGAATAGGAAGAGTGCCAAGGAACCCCTCAAGGAGGAGACCCTCCAT 1205 11081 GACCCAAGGAATTGCAGGTTCCTAAGAACAACTCCCATCCCATCGAGGAGACTTGCAGGATTCCCAAGAAGAACTCCCCATCCAAGAAGATGCTTTAAAAACTTGCAGGATTCCTAAGAACAATCCCCATCCCATCGCAGGCTTTAAAAAAAA

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COMPUTER: 18.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Geneticch) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/99,741 FILING DATE: 26-No. 6100076-1997 CLASSIPRCATION 143: APPLICATION DATA: APPLICATION NUMBER: 08/792498
 GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
COUNTY: SOuth San Francisco
STATE: California
                                                                                                                                                                                                                                                                                               APPLICATION
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODGAG, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041
TELECHONICATION INFORMATION:
TELEPHONE: 650/255-1489
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1300 base pairs
TYPE: Nucleic Acid
STRANDENDESS: SIngle
                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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546 CAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGGCCCA 605
                                                           665
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                                                       GATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTG
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Sequence 4, Application US/08978741 Patent No. 6100076

US-08-978-741-4 ; Sequence 4, Appl ; Patent No. 6100

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675 600 735 660 795 720 855 780 915 940 975 900 1035 1035 1140 1215	
675 600 735 660 795 720 855 780 915 940 915 940 1035 1035 1035 1040 1155 1140	•
675 600 735 660 795 720 855 780 915 940 915 940 1035 1035 11020 11155 1140	72
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675 600 735 660 795 720 855 780 915 940 975 900 1035 1035 1020 1155 1140	661
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CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 1035 AAAGGGAAGGTGAAGGTGGGCGGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 1095 CGGGAGCGGGACCTCCAGGGGAGGCGTCTTCTTCGGCATGGACAGGCCCCCTAAG 1080 ö 180 300 435 GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360 600 099 720 780 840 975 900 960 195 120 255 315 240 375 420 555 480 615 540 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGAGCCCCAGCTCCCCGTCCTAGAG 675 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGAGAG 735 795 855 915 60 ACCTTGGCTGTCCCTTCGTTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG GAAGGAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGAG CTITITACAGGCATITCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC ATGCCCGCGGGGCTCCTGGACCCGGCTACTGCTCTACTGCCCTGCATGGGCGC **ACCTITGGCTGTCCCTTCGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC** CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGGCCCAAGTTCCCCGTCCTAGAA GAACACACACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAG GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC GACTGGAAGAAGCCCTGTGCCATGCTGAAGGACGGACTGCAGGAGGTCGCACTTCATGGCC CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCCAGGTCGACCTGTACATC ATGCCCGCGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCTGCATGGGGCGC CTITITIACAGGCATTICCTICAGIGCTICCTACAGAGAACAAIGGAGCCAGAGAITTICI Gaps . 0 1; Indels Similarity 99.9%; Pred. No. 0; 4; Conservative 0; Mismatches

241 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCCCCTGAGAAGCGGGTG 300 [	421 421 481 541 541 601	601 661 721 721 781 781		1081 SULT 9 -09-333-729A Sequence 16, PRACENT NO. 6 PRACENT NO. 7 APPLICANT: TITLE REPRETED THE
3     3     4     3     4     3     4     3     4     3     4     3     4     3     4     3     4     3     4     3     4 <td>8 8 8 8 8 8</td> <td>8 6 8 6 8 6 8</td> <td>6 B 6 B 6 B 6 B 7</td> <td>dd RR USES</td>	8 8 8 8 8 8	8 6 8 6 8 6 8	6 B 6 B 6 B 6 B 7	dd RR USES
Db   1156   CGGGAGCGGGACCTCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAG   1215   QY   1081   CTGCGGGACGGACTCTGATTCTGGCCGGAGCACCAGACCTCTGATCCTGGAGGGACCAG   1140   Db   1216   CTGCGGGACGAGTTCTGATTCTGGCCGGAGCACCAGACCTCTGATCCTGGAGGACCAG   1275   QY   1141   AGTCTGAGCTGGTCCTTCAGCCAG   1165   QY   1141   AGTCTGAGCTGCTCTTCAGCCAG   1165   Db   1276   AGTCTGAGCTGGTCCTTCCAGCCAG   1300   Db   1276   AGTCTGAGCTGGTCCTTCCAGCCAG   1300   DC   1276   AGTCTGAGCTGCTCCTGCCAG   1300   DC   1276   AGTCTGAGCTGGTCCTTCCAGCCAG   1300   DC   1276   AGTCTGAGCTGGTCCTTCCAGCCAG   1300   DC   1276   AGTCTGAGCTGGTCCTTCCAGCCAG   1300   DC   1276   AGTCTGAGCTGGTCTTCCAGCCAG   1300   DC   1276   AGTCTGCTGCTTCTTCTTCTTCTTTCTTTCTTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTT	WS-08-978-741-16  1S-08-978-741-16  Sequence 16, Application US/08978741  Sequence 16, Application US/08978741  Sequence 16, Application US/08978741  SEQUENCE 1000	COMPUTER READABLE FORM:  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: WinPatin (Genentech)  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/978, 741  FILING DATE: 26-No. 6100076-1997  CLASSIFICATION: 435  PRIOR APPLICATION: 08/792498  FILING DATE: 31  ATTORNEY/AGENT INFORMATION:  MATTORNEY/AGENT INFORMATION:  NAME: SYODOGA, CTA13 G.  NAME: SYODOGA, CTA13 G.	REFERENCE/DOCKET NUMBER: P1011P1  TELECOMMUNICATION INFORMATION: TELEFAX: 650/225-1489  TELEFAX: 650/225-1489  TELEFAX: 650/25-1489  INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ DID NO: 16: SEQUENCE CHARACTERISTICS: TOPOLOGY: Linear TOPOLOGY: Linear US-08-978-741-16  Query Match  Query Match  T2.7%; Score 1100; DB 3; Length 1100; Best Local Similarity 100.0%; Pred. No. 0; Matches 1100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Oy 1 ATGCCCGCGGGCTCCTGGGGTTACCTGCTCTGCATGGGGGGC 60	Db 1 ATGCCCGCGGCTCCTGGCTTACCTGCTCTACTGCCCCTGGTGGGCCC 60 Qy 61 TTGGGAACCAGGCCGTTCTTGGGCTCTCTGCGCTTACTGCCCCTGGTAGGGCCC 60 Db 61 TTGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTGCAAAGCTGCTAAACCGT 120 Qy 121 ACCTTGGCTGTCCTCTTGGATTGAGTACCAGAGTCACAAGCTGCTTCACCAACCTC 180 Db 121 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATCACAAGCCTCTTTCACCAACCTC 180 CATGTGTGTCTACCAGAAGTTCTTAGGTACCAGCATCACAAGCCTCTTTCACCACACCTC 180 Db 181 CATGTGTCTACCAGAAGTACTTCAAGCTGCAGCCTCCTTTCACCAGGCTATCCACAGGCTTACCAACGGGTCATC 240 Db 181 CATGTGTCTACCAGAAGTACTTCAAGGCTGCAGGCTTACCATCGGGGTCATC 240 Db 181 CATGTGTCTACCAGAAGTACTTCAAGGCTGCAGCCTCCCAGGCTTACCATCGGGGTCATC 240

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Pred. No. 6.1e-41;
0; Mismatches 485;
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TITLE OF INVENTION: NUCleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-270-767-14353
US-09-270-767-14353, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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Best Local Similarity 51.6%;
Matches 564; Conservative (
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
       1997-11-26
; PRIOR FILING DATE: 1997; NUMBER OF SEQ ID NOS: 2; SEQ ID NO 16; LENGTH: 1100; TYPE: DNA; ORGANISM: Homo Sapien US-09-333-729A-16
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7336-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 998
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TITLE OF INVENTION: No.1eic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: No.1eic Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13022
LENGTH: 2034
228 CACTCTACCGGAGCTCTGCATGCCCTCCAAGGAGGAGGATCATCCGCCAGCTAAAGAGAA
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Patent No. 6703491
GENERAL INFORMATION:
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US-09-270-767-28905
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Sequence 30507, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
LENGTH: 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTTTTGGGCATTCATCTGCGCAACGGTATCGATTGGGTGAGAGCCTGTGAGCACGTCA
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49.5%; Pred. No. 1.7e-08;
Live 0; Mismatches 218; Indels 12;
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; ORGANISM: Drosophila melanogaster
US-09-270-767-30507
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US-09-270-767-30507
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FACELIA NO. '98124309;
FACELIA NO. '98124309;
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 06/241,755
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOFTHARE: PESESEQ for Windows Version 4.0
SEQ ID NO 12127
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; Sequence 16285, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILLE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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                                                                                                   Query Match 3.9%; Score 58.6; DB 4; Length 2034; Best Local Similarity 60.2%; Pred. No. 4.4e-07; Matches 97; Conservative 0; Mismatches 64; Indels 0
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100.0%; Pred. No. 1.2e-05;
tive 0; Mismatches 0; Indels
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; Sequence 12127, Application US/09949016
; Patent No. 6812339
                      ; ORGANISM: Drosophila melanogaster
US-09-270-767-13022
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Best Local Similarity 100.0
Matches 56; Conservative
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US-09-949-016-16285/c
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ORGANISM: Human
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TYPE: DNA
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Scoring table:

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Perfect score:

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Sequence 603. Apply Sequence 603. Apply Sequence 1986. Apply Sequence 19437. A Sequence 19437. A Sequence 18160. A Sequence 18160. A Sequence 18189. A Sequence 18189. A Sequence 18189. A Sequence 18189. A Sequence 17287.
disk
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: Unknown>
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Sequence 1, Application US/09774954

Publication No. USCO040241645A1

GENERAL INFORMATION:

TITLE OF INVENTION: O-Fucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco

STREET: California
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US-10-278-698-638
US-10-247-671-64
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
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Sequence 4752, Ap
Sequence 7, Appli
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Sequence 5, Appli
                                                                                                                         November 9, 2005, 08:00:04; Search time 1355.3 Seconds (without alignments) 9238.165 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
| CGn2_6/ptodata/1/pubpna/US10B_PUBCOM
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-774-954-5
US-10-301-822-168
US-10-956-157-4752
US-09-774-954-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1514 1512.4 1510.8 1510.8

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Sequence 465, A Sequence 11732, Sequence 190, A Sequence 1 Sequence 4

Sequence

Sequence

Sequence

Sequence 236, App Sequence 1944, Sequence 1941, A Sequence 3, Appli Sequence 41154, A Sequence 114097, Sequence 112, App Sequence 112, App Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 1347, Appl Sequence 31476, A Sequence 31476, A Sequence 31476, A Sequence 31476, A Sequence 317, Appl

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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US-09-774-954-5
US-09-774-954-5
| Sequence 5, Application US/09774954
| Publication No. US20040241645A1
| GENERAL INFORMATION:
| APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-FUCOSyltransferase NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
| COUNTRY: USA
| ZIP: 94080 | COUNTRY: USA
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ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: P1041P1
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 Dass pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                            Score 1514; D; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                  TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 1514; Conservative 0;
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Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.,
APPLICANT: Guillemette, Tracy L.,
APPLICANT: Kamatkar, Shubhangi,
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.,
APPLICANT: Thibodeau, Stephen N.
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                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGIGSTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1512.4;
Pred. No. 0;
0; Mismatches
int Application data:
Pblication Number: Us/09/774,954
Filing Date: 30-Jan-2001
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 11284 base pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
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Best Local Similarity 99.9%;
Matches 1513; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
  CURRENT
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Sequence 4752, Application US/10956157
Publication No. US20050118625A1
GENERAL INPORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH-
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: 120/4-10-04
NUMBER OF SEQ ID NOS: 319805
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   GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
                                                                    CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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US-10-956-157-4752
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, ATTILE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THEARPY OF COLON CANCER
FILE REPERENCE: MPMOIL -0.292PXNN
CURRENT APPLICATION NUMBER: US, 10/301,822
CURRENT FILING DATE: 2001-12-1
FRIOR APPLICATION NUMBER: US, 60/339,971
FRIOR APPLICATION NUMBER: US, 60/331,978
FRIOR FILING DATE: 2002-05-50
FRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FRACE FOR Windows Version 4.0
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ORGANISM: Homo Sapiens
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US-10-301-822-168
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Publication No. US20040241645A1
GENERAL INFORMATION:
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
STATE: 94080
COMPTER READABLE FORM:
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COMPUTER: 1BM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-DAV-1997
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TICTGCTCTTCTGGGAATTTCTCACACTGGCAAAGCAGTCCAGCCTCCGTCTTCTGGTCC 1385
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                                                                                                                                     GGGGACCTCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAGCTGCG
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 781 GGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGG
                                                                         CCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGA
                          GAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGG
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US-09-774-954-4

| Sequence 4', Application US/09774954
| Sequence 4', Application No. US20040241645A1
| Publication No. US20040241645A1
| GENERAL INFORMATION:
| APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: A STREW OF TOTAL STREET: 1 DNA Way
| CITY: South San Francisco STATE: California COUNTRY: USA TTO: 94080
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATA:
FILING DATE: 30-Jan-2001
CLASSIFCATION: «UNKNOWN»
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
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1441 ATTGAATTC 1449
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NAME: Svoboda, Craig G.
RECISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
FELECOMMUNICATION INFORMATION:
FELEPONE: 650/552-1489
FELEPAX: 650/552-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FYER: NUCLESC ASIG
STRANDEDNESS: SINGLE
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-774-954-7
                                                                                                                                                                                    Query Match
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches
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                     CTGCCTGAACGTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
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ADDRESSE: Genetical Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetich)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/08/792,498
FILING DATE: 32-MN-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CTAIG G.
REGISTRATION NUMBER: 109/1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09774954
Publication No. US200404241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
ITITLE OF INVENTION: O-PLOCOSYltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P1041P1 TELECOMMUNICATION INFORMATION:
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TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Single
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US-09-774-954-16
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FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-74N-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-1489
TELEFAX: 650/25-2981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1300 base pairs
TYPE: Nucleic Acid
STAPE: Nucleic Acid
STAPE: Nucleic Acid
STAPE: STAPES: Single
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Best Local Similarity 99.9
Matches 1164; Conservative
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US-09-764-891-6032
US-09-764-891-6032
Sequence 6032, Application US/09764891
Fublication No. US2003007780841
Fublication No. US2003007780841
SERVERLA INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
FPIOR application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIN Ver: 2.0
LENGTH: 10331
TYPE: DNA
TYPE: DNA
COGANISM: Homo sapiens
US-09-764-891-6032
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40.2%; Score 608.6; DB 10;
Best Local Similarity 98.6%; Pred. No. 5.4e-186;
Matches 614; Conservative 0; Mismatches 9;
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                                    DB 11; Length 1100;
                                                        0; Indels
                                 Query Match 72.7%; Score 1100; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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JS-09-774-954-16
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PLILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 22744
                                                                                                                                                                                                  Score 471.4; DB;
Pred. No. 9e-142;
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 442.8;
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFWARE: PatentIn version 3.2
SEQ ID NO 4751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-918-995-22744
US-09-910-22744, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1) ... (477)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                  31.1%;
99.8%;
                                                                                                                                                                                                Query Match 31.1
Best Local Similarity 99.8
Matches 472; Conservative
                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-956-157-4751
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                                                                                                  LENGTH: 1506
                                                                                                                    TYPE: DNA ORGANISM: 1
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                                                                                                                                        Sequence 9986, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth World:

APPLICANT: World:

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM THAITIS AND HUMAN PROTEASES

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT APPLICATION NUMBER: US/10/956,157

NUMBER OF SEQ ID NOS: 319805

SOPTWARE: Patentin Version 3.2

SEQ ID NO 9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4751, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 471.4; DB 22; Length 1400;
Pred. No. 8.7e-142;
0; Mismatches 1; Indels 0;
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                    1514
                                            6727 GGTTTTTGAAATCATTGAATTC 6749
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Best Local Similarity 99.8%;
Matches 472; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo Bapiens
                                                                                                                                US-10-956-157-9986
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US-11-U97-143-18161

Sequence 18161, Application US/11097143

Publication No. U52005020858A1

GENERAL INFORMATION:
APPLICANT: Venter. J. Craig
APPLICANT: Venter. J. Craig
APPLICANT: Venter. J. Craig
APPLICANT: Venter. D. Craig
APPLICANT: Venter. J. Craig
TITLE OF INVENTION: DRGSOPHILA GENES.
FILE REFERENCE: CLO00728
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: 00/15/332
FRIOR APPLICATION NUMBER: 60/15/332
FRIOR FILING DATE: 1999-10-19
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 1999-10-19
FRIOR FILING DATE: 1999-10-19
FRIOR FILING DATE: 1999-10-28
FRIOR APPLICATION NUMBER: 60/164,769
FRIOR APPLICATION NUMBER: 60/164,769
FRIOR FILING DATE: 1999-10-28
FRIOR APPLICATION NUMBER: 60/164,769
FRIOR FILING DATE: 1999-10-28
FRIOR FILING DATE: 2000-01-12
FRIOR FILING DATE: 2000-01-12
FRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                    1228 AGAGTGCCAGGGACCCCTCAAGGAGGGAGACGCTCCATATCCCCAGGGCATAGGACTTGCA 1287
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                               211 TCTTCTTTCTTCGGCATGGACAGGCCCCTAAGCTGCGGGACGACGAGTTCTGATTCTGGCCC
                                                                                                  CTGGCAGCCAGAGGTGCTCCGGGATTGCAAACTCCTCTTCTCACCTGCCAAAGATGGAGA
  1048 TCTTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGAGTTCTGATTCTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: DROSOPHILA
US-11-097-143-18161
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US-11-097-143-18161
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Best Local S:
Matches 563
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                                                                                                                                                                                                                                                                             CCACTITATIGGCAACTGTGTCTCCTTCCTTGCGCTTTGTGAAGCGGGAGCGGGACCT 1034
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                                                                                                              190 CCAGGGGAGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCGGGAGTT
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                                                                                                                                                                              915 GGTGGTGAGCCTGAAGCCTGAGGTGGCCCAAGTCGACCTGTACATCCTCGGCCAAGCCGA
                                                                                                                                                                                                                                                                                                                130 CCACTITATIGGCAACIGIGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGGAGCGGGGCTT
                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.1%; Score 441; DB 10; Length 479; Best Local Similarity 98.9%; Pred. No. 4e-132; Matches 444; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-918-95-19437
Sequence 19477, Application US/09918995
Publication No. US2003007362341
Fublication No. US2003007362341
FUBLICANT: Hyeaq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PAPLICATION NUMBER: US/09/918,995
CURRENT PELLING DATE: 2001-07-30
FRIOR PRIOR APPLICATION NUMBER: US/09/235,076
FRIOR PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SSEQ ID NOS: 38054
SSEQ ID NO 19437
LENGTH: 479
Best Local Similarity 98.1%; Pred. No. 1e-132;
Matches 458; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-19437
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Pred. No. 3.6e-37;
); Mismatches 476;
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: ARRAYS, FOR DETECTING EXPTITLE OF INVENTION: ARRAYS, FOR DETECTING EXPTITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PRILORION NUMBER: GO/160,191
PRIOR PRILOR DATE: 1999-10-19
PRIOR PRILOR DATE: 1999-10-19
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-12-28
PRIOR PRILOR DATE: 1999-12-28
PRIOR APPLICATION NUMBER: GO/175,693
PRIOR APPLICATION NUMBER: GO/175,693
PRIOR PRILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GO/194,831
PRIOR PILING DATE: 2000-01-2
PRIOR PILING DATE: 2000-01-2
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PRIOR FILING DATE: 2000-03-23
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SOFTWARE: FastSEQ for Windows Version 4.0
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RESULT 14
US-11-097-143-18160/c
; Sequence 18160, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

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Search completed: November 9, 2005, 15:51:13 Job time : 1357.3 secs
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US-09-783-590-11501
US-09-783-590-11501
Sequence 11501, Application US/09783590
Fatent No. US2002010850A1
GENERAL INFORMATION:
Haseltine, William A.
APPLICANT: Dillon, Patrick J.
APPLICANT: Li, Hadong M.
APPLICANT: Rosen, Craig A.
TITLE REPERENCE: PO-16.201
TITLE REPERENCE: PO-16.201
TITLE REPERENCE: PO-16.201
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 1995-04-12
FRICH PRILING DATE: 1995-04-12
FRICH PRILING DATE: 1994-11-21
FRICH FILING DATE: 1994-11-21
FRICH FRICH FILING DATE: 1994-11-21
1264 Gredicariadacricia arcacarga ir gerida acracació cirra de cardedec 1205
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1144 TCGAACCACTITATCGGCAACIGIAITCCTCTTACTCGGCATTCGAAAAAGGGAACGA 1085
                                                                                                                                                                                                                                                         1384 cgriedraczacztarceggagerergeargecerecaaggaggegareareaecagera 1325
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                                                                                                                                                   1444 CACGTCAAGGATAGCCAGCATCTGTTTGCCTCGCCGCAGTGCTTGGGGTTAAAAATGAA 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      913 AAGGTGGTGAGCCTGAAGCCTGAGGTGG---CCCAAGGTCGACCTGTACATCCTCGGCCAA 969
                                                                                                      682 ATGCTGAAGGACGG-----GACTGCAGGCTCGCACTTCATGGCCTCTCCGCAGTGT 732
                                                                                                                                                                                                            AAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTCGGTCTAC 852
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NAME/KEY: misc feature
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (46)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (46)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (222)
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LOCATION: (9)
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Best Local Similarity 83.9%; Pred. No. 5.7e-26;
Matches 177; Conservative 0; Mismatches 23;
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (301)
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LOCATION: (320)
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NAME/KEY: misc feature
LOCATION: (333)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (342)
NAME/KEY: misc feature
LOCATION: (374)
NAME/KEY: misc feature
LOCATION: (386)
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NAME/KEY: misc feature
LOCATION: (390)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (400)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (400)
COTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11501
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AK0081059 Wus muscu
BX34598 BX345988
BQ677046 AGRICOURT
BM900055 AGRICOURT
BM345989 BX345989
AL135434 BKFZp7620
BI524031 60305202
BX449172 BX449172
BM477212 AGRICOURT
CO774833 ILLUMIGEN
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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RESULT 1	
1.00110	
DEFINITION	CK61/950 full-length cDNA clone CSOD/1008YF12 of T cells (Jurkat cell line)
	Cot 10-normalized of Homo sapiens (human).
ACCESSION	CR617950
VERSION	CR617950.1 GI:50498757
KEYWORDS	U
SOURCE	Homo sapiens (human)
ORGANISM	
	etazoa;
	Primates;
REFERENCE	1 (bases 1 to 1555)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://filllongth inmitrocon com/ InVitroCon Composition 1600
	netri)/raintempentingentogenteem/ invitablem torporation root Paradav Avenue
REFERENCE	2 (bases 1 to 1555)
AUTHORS	noscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
	NCE (
	- Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
	end enriched, double-strand cDNA was digested with Not I and cloned
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
	was normalized. Library was constructed by Life Technologies, a
	division of Invitrogen.
FEATURES	Location/Qualifiers
source	11555
	/organism="Homo sapiens"
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	/tissue_type="T cells (Jurkat cell line) Cot
	10-normalized"
	/plasmid="pCMVSPORT 6"
ORIGIN	
Query Match	95.4%; Score 144
Best Local	Similarity 99.9%; Pred. No. 0;
Matches 1445;	vative 0, Mismat
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AGTCTGAGCTGGTCCTTCCAGCCAGGCCTGGCAGGCCAGAGGTGCTCCGGGATTGCAAACT
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Best Local Similarity 92.8
Matches 952; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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                                                            ACCTTGGCTGTCCCTTCGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 180
                                                                                                     CATGIGICCIACCAGAAGIACTICAAGCIGGAGCCCCTCCAGGCTIACCAICGGGICAIC 240
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ATGCCTGCGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC 168
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1009 AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGCCCAGGTCGACCTGTACATC
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CB 1 (bases 1 to 1141)

RS 11,W.B., Gruber,C.; Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30371746.

Contact: Genoscope
Contact: Genoscope
Contact: Genoscope.

Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EWY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EWY cedex is in the tarand cDNA was primed with a Not-1c-1ggo(GT) primar. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX353274 Homo sapiens NETBOBLASTOWA COT 25-NORWALIZED Homo sapiens
cDNA clone CSODC003YJ11 5-PRIME, mRNA sequence.
BX353274
BX353274.2 GI:46290116
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/mol_type="maxNa"

/db Arzef="Lexacn.9606"

/clone="CSODC003YJ11"

/tissue type="MERROBABASTOWA COT 25-NORWALIZED"

/clone lib="Homo sapiens NEUROBLASTOWA COT 25-NORWALIZED"

/note="Ist strand cDNA was primed with a NotI-oligo(dT)

primer. Pive prime and enriched, doubbe-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."
TCCATATCCCAGGGCATAGGACTTGCAGGTTCCTAGGAGGAGGAGGAGCATCTCCCATCGCAC
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                                                                                                                                            CCTCTTCTCACCTGCCAAAGATGGAGAAGAGTGCCAGGGACCCCTCAAGGAGGGGAGACGC
                                                                                                                                                                                                                                    TCCATATCCCAGGCCATAGGACTTGCAGGTTCCTAGGAGCAGGAGCATCTCCCATCGCAC
                                                                                                CCTCTTCTCACCTGCCAAAGATGGAAGAGTGCCAGGGACCCCTCAAGGAGGAGGACGC
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AK081059  AK081059  Mas musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930076G19 product:protein O-fucosyltransferase 1, full insert sequence. O-fucosyltransferase 1, full insert sequence. AK081059.1 GI:26095647  HTC; CAP trapper. Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (hordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus Larninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning 99279553 10349636	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 31042159	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishil, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer 20530913		Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawat,J., Kodima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,A., Murata,M., Nakah,J., Kodima,Y., Rondo,S., Konno,H., Murata,M., Nakah,K., Namazaki,R., Ohno,M., Ohsato,N., Ohazaki,Y., Satho,R., Satoh,H., Sakai,C., Sakazume,N., Sano,H., Sasati,D., Shibata,R., Shinagawa,A., Shiraki,T. Sakazume,N., Sogabe,Y., Tanaka,T., Tomaru,A., Takahashi,P., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki, Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Toya,T., Yasunishi,A., Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-045, Japan (E-mail:genome-reseggs.riken.ip, Vokohama, Kanagawa 230-045, Japan (E-mail:genome-reseggs.riken.ip, URL:http://genome-georiken.ip/, Tel:81-45-503-9222, Fax:81-45-503-9216)
RESULT 3 AKO81059 LOCUS DEFINITION ACCESSION VERYORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE PUBMED	KEFEKENCE AUTHORS TITLE JOURNAL MEDELINE PUBMED REFERNCE	AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL
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1 ATGCCGCGGGCTCCTGGGACCCGGCTTACTGCTCTACTGCCCCTGCATGGGGGCGC (	GCATACTGCTTTGAGGTGGCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG [	CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT		TCTT                :     :     :     :     :     :

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AKO44629 2616 bp mRNA linear HTC 03-APR-2004 Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930028F21 product:protein O-fucosyltransferase 1, full
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AKO44629.
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GI:26336652
Mus musculus (house mouse)
Mus musculus (craniata; Vertebrata; Buteleostomi;
Musmaryota; Metazoa; Chordata; Craniata; Vertebrata; Musinae; Musmania;
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                                                                                                                                                                                                                                                                         GGGATGAATTTTGATCCCATCTGAAGCCCCCACCTCCC-----
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High-efficiency Full-length cDNA cloning
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     Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues:

URL:http://genome.gsc.riken.jp/
URL:http://genome.gsc.riken.jp/
Location/Qualifiers
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wattahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enriched mouse cDNA library"
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Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2616)
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O-fucosyltransferase 1 (MGD|MGI:2153207, GB|NM_080463,
evidence: BLASTN, 99%, match=1290)
                                                                                                                                                                                                                                                        Genome Exploration Research Group Phase II Team and
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COMMENT

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VSLKPEVAQIDLYILGQADHFIGNCVSSFTAFVKRERDLHGRQSSFFGMDRPSQLRDE
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(Dasses 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                    AGCGGCCCCCTCACGATGACTATGTGCCTGCCTGACCTGAAGGAGATCCAGAGGGCTGT
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815 TGTGGGCATTCATCTGCGCATTGGCTCTGACTGGAAGAACGCCTGTGCCATGCTGAAGGA
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                                                                                                                                                                                                                                                            BX345988 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED HOmo sapiens cDNA clone CSODJO08YF12 3-PRIME, mRNA sequence.

BX345988
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(cell line="JURKAT"
(clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
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.larity 99.4%; Pred. No. 4.1e-227;
Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                        1083 GCGGGACGAGTTCTGATTCTGGCCGGAGCACCAGACCCTC 1122
                                                                                                                                                                                         1200 TCGGGATGAATTTTGATCCCATCTGAAGCCCCCACCTCCC 1239
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJ008YF12"
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10-NORMALIZED"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                               721 CAAAGCAGTCCAGCCTCCGTCTTCTGGTCCACTCTGCTCTGAGCAGCCTGGGATGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                        CTCTTCAGAGAGATTTTTTTATAGAGATTTTCTATAATTTTTGATACAAGGTCATGACTA
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can kfound through the I.M.A.G.E. Consortium/LLNL at:
Phitp://mage.llnl.gov
Plate: LLCM1904 row: e column: 14
High quality sequence stop: 629.
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Pred. No. 7.4e-195;
0; Mismatches 54;
                                                                                                           GGAGCAGGAGCATCTCCCATCGCACGTGCTTTCTGCTCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ilarity 93.0%;
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/tissue_type="melanotic melanoma, cell line"
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/tissue_type="melanotic melanoma, cell line"
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                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lead through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LCCA1453 row: h Column: 21
High quality sequence stop: 662.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BX345989.2 GI:46549776
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Homo sapiens agains
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
Li, W B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                        GTGGCATACTGCTTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATG
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On May 5, 2003 this sequence version replaced gi:30377055. Contact: Cenoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefe@qenoscope.cns.fr, Web: www.agenoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pCMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="taxon"
/db_xref="taxon"
/clone="CSOD7008YF12"
/cell_type="T_CELLS (JURKAT_CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T_CELLS (JURKAT_CELL LINE) COT
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DKFZp76200115_x1 762 (synonym: hmel2) Homo sapiens cDNA clone
DKFZp76200115_5', mRNA sequence.
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I (bases 1 to 719)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research CORTEX; Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin.
6, 14059
GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT
                  GSCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT
                                                     GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTCCAGGCTCGCACTTCATGGCC
                                                                                 768 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
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/lab_host="DH10B"
/clone_lib="762 (synonym: hmel2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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0
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No s1 sequence available.
This clone (DKFZp76200115) is available at the RZPD in Please context the RZPD: Ressourcentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 717.4; DB 1; Length 719; Pred. No. 1.2e-187; 0; Mismatches 1; Indels 0
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/clone lib="NIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
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1 (bases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11505 row: d column: 01
High quality sequence stop: 880.
Location/Qualifiers
241 GGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCCATTGGCTC
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/db_xref="taxon:9606"
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BI524031.1 GI:15348823
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo.

Bukaryota, Matheria; Primates; Catarrhini, Hominidae, Homo.

E 1 (bases 1 to 898)

Li, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

M. Unpublished (2001)

On May 22, 2003 this sequence version replaced gl:31030014.

Contact Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENKz cedex - FRANCE
Email: seqref@genoscope.ons.fr. Web: www.genoscope.ons.fr

Ist strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was Gigsted with Not I and cloned into the Not I and EcoRv Sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. Library was constructed by Life Technologies, a This sequence belongs to sequence cluster 9980.f

For more information about this cluster, see http://www.genoscope.cns.fr/dnafs=CSOAMO14AF06GP1&c=9980.f.
   BX449172.2 GI:47067286
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anonymous pool of 24 week female lung, 16 week female spleens, and 20-22 week male spleens. Library is oligo-dry primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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47.0%; Score 712.2; DB 4; Length 889;
Best Local Similarity 99.1%; Pred. No. 3.7e-186;
Matches 758; Conservative 0; Mismatches 3; Indels 4,
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/organism="Homo sapiens"
//organism="Homo sapiens"
//mol type="mRXN"
//db xref="taxon:9606"
//clone="CSODMO14YK11"
//tssue_type="FETAL LIVER"
//clone_lib="Homo sapiens FETAL LIVER"
//ore="Organ: liver: Vector: pCWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BCORV sites of the pCMVSPORT 6 vector: Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCTGAGAAGCGGGTG 300
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                                                                                                                                                                                                                                                                                                                                                                1arity 97.8%; Score 706.6; DB 5; Length 898; Pred. No. 1.38-184; Conservative 4; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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BX449172 988 bp mRNA linear EST 06-MAY-2004 BX449172 Homo sapiens FETAL LIVER Homo sapiens CDNA clone CSODMO14YK11 5-PRIME, mRNA sequence.

LOCUS RESULT 11 BX449172

ACCESSION

302

1036

976

1156

1216

422

1336

542

1396

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1397 AGCAGCCTGGGATGCTGAACTCTTCAGAGATTTTTTTATAGAGAGATTTCTATAATTT 1456
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Sequenced on 2004.07.21. 611 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                          AAAGAIGGAGAAGAGTGCCCAGGGACCCCTCAAGGAGGAGAGGCCCCCTATACCCAGGGCA
                                                                                                           123 TGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGTCTATACATCCTCGGCCAAGCCGACC
                                                                                                                                                        977 ACTITATIGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGGACCTCC
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                      CTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAGG
                                                                                        TGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACC
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ILLUMIGEN MCQ_51950 Katze_MNLV Macaca nemestrina cDNA clone IBIUW:29960 5' similar to Bases 7 to 852 highly similar to POFUTI (Hs.178292), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca nemestrina (pig-tailed macaque)
Macaca nemestrina
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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1 (bases 1 to 942)

Karze, M.G.

Larges, G.B.

Unpublished (2003)

Contact: C. Magness

11lunigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATACAAGGTCATGACTATCCTAGAA 1483
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Homo sapiens cDNA clone IMAGE:5559347
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12283 row: m column: 12
High quality sequence stop: 685.
CTITITIACAGGCATTICCTICAGIGCTICGIACAGAGAACAAIGGAGCCAGAGATTITCT
                                               TGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGC
                                 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGCCCCAGCCCAGTTCCCCGGTCCTAGAA
                                                                                                   GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACG-AAATGGTGAAGACGGGAGA
                                                                                                                                                                      600 GGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 704)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                          CT-CTCCGCAGTGTGTGGCTACAGCCGCAGCACAGCGGCC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 683.8; DB 4;
Pred. No. 2.7e-178;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT 6477457 NIH_MGC_88 15, mRNA sequence.
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BM475212.1 GI:18524254
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ilarity 99.7%;
Conservative
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Homo sapiens
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Best Local Similarity
Matches 685; Conserv
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                                                                                                                                    678
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AUTHORS
TITLE
JOURNAL
COMMENT
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BM475212
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KEYWORDS
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Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 808)

2 1 (bases 1 to 808)

3 NIH-MGC http://dgc.nci.nih.gov/.

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

6 Email: cgapba-r@mial.nih.gov

7 Tissue Procurement: ArCc

6 CDNA Library Preparation: Ling Hong/Rubin Laboratory

6 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

7 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8 found through the I.M.A.G.E. Consortium/LLNL at:

9 found through the I.M.A.G.E. Consortium/LLNL at:

9 found through the I.M.A.G.E. Consortium/LLNL at:

1 fo
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//nol type="mRNA"
//db Zref="texon:9606"
/clone="IMAGE:4842061"
/tissue Lype="normal pigmented retinal epithelium"
/lab host="DHIOB (phage-resistant)"
/lone=lib="NHH MGC 43"
/hote="Organ: eye; Vector: poTB7; Site_1: Xhol; Site_2: Mote="Organ: eye; Vector: poTB7; Site_1: Xhol; Site_2: Cloned into EcoRI/Ahol sites using the following 5' adaptor: GGCACGAG (G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of california, Berkeley) using AAP-CNA synthesis Kit (Stratagene) and Supersoript II (Stratagene) and Supersoript II (Iffe Technologies).
Note: this is a NIH_MGC Library. |"
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602705255F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842061 5',
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755 CTGACTGGAAAATGCCTGTGCTATGCTAAAGGACGGAACTGGCAGCTCGACTTTCTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BG747760.1 GI:14058413
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Homo sapiens
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                                                                                                                                                                                                875 GTGCCTGCCT 884
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BG747760
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Matches 69
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VERSION
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SOURCE
ORGANISM
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGTTCCCCGTCCTAGAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 ATGCCGCGGGCTCCTGGGACCCGGCTAACTGCTCTACTGCCCCTGCATGGGGCGC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TITIGGGAACCAGGCCGAICACTICTIGGCCICTCTGGCATITIGCAAAGCTGCTAAAACCGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCCCCTGGCCCCCTGAGAAGCGGGTG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCCAGATAAGAAGACGTGCCCCATGAAG 360
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                                                                                                                                                                                                                                                                                                                                                                                   /sex.male...
/lab.host="Blectromax DH10B"
/lab.host="Blectromax DH10B"
/clone lib="Katze_MNLV"
/note="Organ: liver; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CATGIGICCIACCAGAAGIACTICAAGCIGGAGCCCCTCCAGGCIIACCAICGGGICAIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.1%; Pred. No. 2.6e-175;
Matches 743; Conservative 0; Mismatches 43; Indels 4.
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/strāin="Indian"
/db xref="taxon:9545"
/clone="IBIUW:29960"
                       PCR PRIMERS
PORMARD: CCCTCACTPANGGGAACAAAA
BACKWARD: CACTACTPANGGGGGAATTGGGTA
INSERT LENGTH: 942 Std Error: 0.00
Plate: CL000531 row: E column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYANNO.
                                                                                                                                                                                                Location/Qualifiers
        http://www.macaque.org
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1. .801
/organism="Sus scrofa"
/organism="Sus scrofa"
/db zref="taxon:9823"
/clone="OVR010034G09"
/tissue_type="ovary"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult ovary"
                                                                                                                                                                                                                                                                                                                                                                                                        TCATGGAGAGAGCTGGCACCCACTGGCCCCCTGAGAGGCGGGTGGCATACTGTTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITCCTTCAGTGCCTCCTACAAAGACCAGTGGATCCAAAGATTTTCTCCCAAAGGAACATC 300
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     on the quality values.
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                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                      43.6%; Score 660.2; DB 5; Length 89.0%; Pred. No. 1e-171; ive 0; Mismatches 88; Indels
 quality bases were trimmed based Location/Qualifiers
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Best Local Similarity 89.0
Matches 713; Conservative
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1 (Joases I to 801)

2 Unases I to 801)

3 Unnishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamaalia, N. and Awata, T.

9 EDBE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

1 Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi

Animal Genome Laboratory, Genome Research Department

Animal Genome Laboratory, Genome Research Department

National Institute of Agrobiological Sciences

2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-838-8627

Email: huenishi@affrc.go.jp

EST project With full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP144264 Eull-length enriched swine cDNA linear EST 30-DEC-2003 BP144264 full-length enriched swine cDNA library, adult ovary Sus screfa cDNA clone OVR010034G09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
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                  322 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCCTGAGAAGCGGGTG
                                                                                                                                           GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGACGTGCCCCATGAAG
                                                                                                                                                            442 GAAGGAAACCCCTTTGGCCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGGGAGA
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                                                                     AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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Search completed: November 9, 2005, 10:38:05 Job time: 5495.13 secs

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AF375885 Mus muscu BC046259 Mus muscu AJ353754 Gallus ga AJ720352 Gallus ga BC08519 Xenopus t AJ781498 Siluzana AJ606070 Fugu rubr AJ51425 Xenopus 1 AJ719585 Gallus ga AJ121897 Human DNA AJ719585 Gallus ga AJ121897 Human DNA AK112708 Ciona int AK124093 Homo sapi AC094844 Rattus no AC194814 Rattus no AC78911 Mus muscu AJ831490 Drosophil AZ8118651 Drosophil AJ18651 Drosophil AJ781501 Drosophil AJ781501 Drosophil

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BD103189 O-fucosyl
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BD103189 O-fucosyl
AR75584 Homo sapi
BD103199 O-fucosyl
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BD103191 O-fucosyl
AR781500 Pan trogl
AR13453 Sequence
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AR34509 Bos tauru
AJ73459 Bos tauru
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1 ATGCCCGGGGCTCCTGGGA......CTGCGGGACGAGTTCTGATT 1100
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

linear PAT 17-OCT-2001		6; Length 1100; ; 0; Indels 0; Gaps 0;	CTACTGCCCTGCATGGGGCGC 60	ATTIGCAAAGCIGCTAAACGGF 120 	CAAGCCTCCTTTCACCAACCTC 180	CCAGGCTTACCATCGGGTCATC 240	CTGGCCCCTGAGAAGCGGGTG 300
AR163457 Sequence 16 from patent US 6270987. AR163457.1 GI:16234062	Unknown. Unknown. Unknown. Unclassified. 1 (bases 1 to 1100) 1 (bases 1 to 1100) Amang, Y. and Spellman, M.W. O-fucosyltransferase Patent: US 6270987-A 16 07-AUG-2001; Location/Qualifiers 1100 /organism="unknown" /mol_type="unassigned DNA"	100.0%; Score 1100; DB nilarity 100.0%; Pred. No. 1e-253 Conservative 0; Mismatches	ATGCCCGCGGGCCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC	TTTGGGAACCAGGCGATCACTTCTGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT	ACCTIGGCTGTCCCTCCTIGGATIGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC	CATGRECCTACCAAAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC	AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCCTGAGAAGCGGGTG
1 57 57 FION ION N	NISM NCE ORS E E NAL ES	ORIGIN Query Match Best Local Similarity Matches 1100; Conser	Oy 1 Db 1	Oy 61 Db 61	Qy 121 Db 121	Qy 181 Db 181	Qy 241
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AX780153 HSM803330 AJ781500

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AR163453 BD103191 AY344580 AJ781503 SSC567917 AJ781499

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                    Unidentified
JP 2001527389-A/9
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JP 2001997 
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1 (bases 1 to 1100)
Wang Y. and Spellman,M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 9 25-DEC-2001;
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QY 721 TCTCCGCAGTGTGGGCTACAGCCGCAGCACAGCGCCCCCCTCACGATGACTATGTGC 780	Oy 781 CTGCCTGACCTGAAGAATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGC 840	Qy         841         CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC         900           Db         841         CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC         900	QY         901 AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC 960           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         96.1 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020           Db         96.1 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAG 1020	Qy         1021 CGGGAGCGGGACCTCCAGGGAGGCCGTCTTCTTTCTTCGGCATGGACAGGCCCCCTAAG 1080	Qy 1081 CTGCGCGACTTCTCATT 1100	AR163451 1514 bp	DEFINITION Sequence 2 from patent US 6270987. ACCESSION AR163451 VERSION AR163451.1 GI:16234056 KEYWORDS	_	AUTHORS Wang, Y. and Spellman, M.W. TITLE O-fucosyltransferase JUNNAL Patent: US 627087-A 2 07-AUG-2001; FRATHERS	rce	Query Match Best Local Similarity 100.0%; Pred. No. 1e-253; Matches 1100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	0y 1 ATGCCCGCGGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGGCG 60	Qy         61         TTTGGGAACCAGGCCGATCACTTCTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT         120           Db         61         TTTGGGAACCAGGCCGATCACTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT         120	9y 121 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 180	Oy 181 CATGIGICCTACCAGAAGTACTICAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATC 240	OY 241 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACC

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CTCGGCCAAGCCGACCACTITAITGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAG 1020
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 721 TCTCCGCAGTGTGTGGGCTACAGCCGCAGAGCGCGCCCCCCTCACGATGACTATGTGC 780
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E 1 (bases 1 to 1300)
S Wang, Y. and Spellman, M.W.
O-fucosyltransferase
O-fucosyltransferase
AL Patent: US 6270897-A 6 07-AUG-2001;
Location/Qualifiers
1007-2007
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Sequence 6 from patent US 6270987.
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               25-DEC-2001
17-DEC-1997 JP 1998532877
31-JMN-1997 US 08/792498,26-NOV-1997 US WANG, MICHAEL W SPELLMAN
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
                                                                                                                           Location/Qualifiers
1. 1514
1. Organism='Unidentified'
Location/Qualifiers
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2001527389-A/1
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PF 17-DEC-1997 JP 1998532877  PR 31-JAM-1997 US 08/792498,26-NOV-1997 US 08/97874  YANG WANG,MICHAEL W SPELLMAN  PC C12N15/54,C12N9/10,C07K16/40  CC Strandedness: Single;  CC Topology: Linear;  CC O-fucosyltransferase  FF Rey  FT SOURCE 1.1300	Location/Qua 11300 /organism="v	/mol_type="genomic DNA" /db_xref="taxon:32644" ORIGIN	Query Match Best Local S Matches 1099	1 136	61 196	Oy 121 ACCTTGGCTGTCCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAAGC	316	Oy 241 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCACTGGCCCCCTGAGAAGCGC	301	Oy 361 GAAGGAAACCCCTTTGGCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCC	OY 421 CTTTTACAGGCATTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTT	Qy         481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGCCCCAGTCCCCGTCCTA	Qy 541 GAACAGGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGGAGAA 	Qy         601         GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGC           Db         736         GCCCAGATTCATGCCCACCTTGTCCGGCCTATGTGGGCATTCATCTGCGCATTGGC	OY 61 GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGTCGGACTTCATG	Db 856 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCAGCGGCCCCCCTCACGATGACTATG
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0; GGGCGC 60 |||||| |GGGCGC 195 AACCGT 120 ||||||| AACCGT 255 AACCTC 180 ||||||| |AACCTC 315 GTCATC 240 |||||| GTCATC 375 CGGGTG 300 ||||||| CGGGTG 435 ATGAAG 360 |||||| ATGAAG 495 TCGGAG 420 |||||| |TCGGAG 555 rttrct 480 ||||||| |rtrcr 615 CTAGAA 540 |||||| CTAGAG 675 3GAGAG 600 |||||| 3GAGAG 735 3GCTCT 660 ||||||| 3GCTCT 795 ATGTGC 780 |||||| ATGTGC 915 ATGGCC 720 |||||| ATGGCC 855 3741 PI Gaps

GNOADHFLGSLAFAKLLNRTLAVPFWIEYOHHKPPFTNLHVSYQKYFKIEPLQÀYHRV ISLEDFMEKIAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFN KSELFTGISFSASYREQWSQRFSPKEHPVLALFGARAQGFPVLEBHRPLQKYMYWSDEM VKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCYGYSRSTAA PLTWTMCLPDLKEIQRAVKLWYRSLDAQSVYVATDSESYVPELQQLFKGKVKVUSLKP EVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRFSSFFGMDRPPKLRDEF"	Query Match 99.9%; Score 1098.4; DB 9; Length 5249; Best Local Similarity 99.9%; Pred. No. 2.4e-253; Matches 1099; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	0y 1 AIGCCCGCGGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60	Qy         61 TITIGGGAACCAGGCCGAICACTITCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 120           179 TITIGGGAACCAGGCCGAICACTTCTTGGGCTCTCTGGGCTTTTGCAAAGCTGCTAAACCGT 238	Qy 121 ACCTIGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTGACCAACCTC 180	35 30	Db 359 AGCTTGGAGGATTTCATGGAGAAGCTGGACCCCACCCACC	361 gaagaahacccrtrrgggarcagtrrcagtrrcargagtrrcargagggggggggg	Qy         421         CTITITACAGGCATTICCTICAGIGCTICCTACAGAGAACACAGAGACCAGAGATTICT         480           Db         539         CTITITACAGGCATTICCTICAGIGCTICCTACAGAGAACAAIGGAGCCAGAGATITICT         598	Oy 481 CCAAAGGAACHTCCGGTGCTTGCCTGCCAGGAGCCCCAGTCCCCGTCCTAGAA 540	OY 541 GAACACACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGAGGGGAGAG 600	Qy 601 GCCCAGATTCATGCCCACCTTGTCCGGCCTTTCATCTGCGCATTGGTTC 660	Qy         661         GACTGGAACGCCTGTGCCGATGCTGAAGGACTGCAGGCTCCACACTCCATCATGGCC         720           Db         779         GACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGACTGCAGGCTCCAGGCTCCATTCCATGGCC         838	Qy         721         TCTCCGCAGTGTGTGGGCTACAGCGCACAGCACCCCCCCC	Qy 781 CTGCCTGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGGGTGAGGTGGCTGGATGCC 840 Db 899 CTGCCTGAAGAAGAGTCCAGAGGGTGTGTGAAGGTGTGGAAGGTGCTGAAGGAGGTGTGTGAAGGAAG		901 AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGCCCAGGTCGACCTGTACATC 960
Oy         781 CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840	901 AAAGGGAAGGTGAAGGTGGTGAGCTGAAGCCTGAGGTGGCCCAGGTC 	Qy 961 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020	Qy         1021         CGGGAGCGGACCTCCAGGGGAGCCGTCTTCTTCTTCGGCATGGACAGGCCCCCTAAG 1080           Db         1156         CGGGAGCGGGACCTCCAGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCTAAG 1215	Qy 1081 CTGCGGGACGAGTTCTGATT 1100 	RESULT 7 AF375884 LOCUS AF375884 S249 bp mRNA linear PRI 23-OCT-2001 DEFINITION Homo sapiens protein o-fucosyltransferase (POFUTI) mRNA, complete		OKCANISM HOMO SEPTEMBY.  BUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.  REFERENCE 1 (Dases I to 5249)  AUTHORS Wang, Y., Shao, L., Shi,S., Harris, R.J., Spellman,M.W., Stanley,P.	and Haltiwanger, R.S. Modication of epidermal growth factor-like repeats with O-fucose. Molecular cloning and expression of a novel GDP-fucose protein O-fucosyltransferase	JOURNAL J. Biol. Chem. 276 (43), 40338-40345 (2001) MEDLINE 21523965 PUBMED 1554432 REFERENCE 2 (bases 1 to 5249)	and Haltiwangery. F.; wangil., suacid.; natissand.; sperimum.r.; sperimum.r.; birect Submission Submitted (02-MAY-2001) Cell Biology, Albert Einstein College Submitted (02-MAY-2001) Cell Biology, Albert Einstein College	-	/mol_type="mRNA" /db_xref="latxon:9606" /chromosome="20" /map="between PLAGL2 and KIF3B"	/tissue type="heart" gene	/gene="bowling"//gene transfer of fucose from GDP-fucose to serine or threonine on epidermal growth factor-like	/note="0-FucT-1; glycosyltransferase" /codon start=1 /product="protein o-fucosyltransferase"	/procein_id="MALD95/6.1" /db_xref="GI:15825114" /translation="MGAAAWARPLGVSFLLLLLPLPGMPAGSWDPAGYLLYCPCMGRF

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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Sequence 13711 from Patent WO
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Obara,O. Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
Submitted (12-1995) Osamu Ohara, Kazusa DNA Research Institute;
Submitted (12-1995) Osamu Ohara, Kazusa DNA Research Institute;
Submitted (12-1995) Osamu Ohara, Razusa DNA Research Institute;
1532-3, Yana, Kasarau, Chiba 292-0812, Japan
(15-18-1-16) Code Library, Tel:+81-438-52-3913)
On May 9, 2002 this sequence version replaced gi:1136419.
Location/Qualifiers
1. 5189
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/note="This sequence was obtained by subcloning of the DNA
derived from two cDNA clones (1 - 1066 was
derived from pf00933 and 1067 - 5189 was derived from
ha02567)."
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The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1 DNA Res. 3 (1), 17-24 (1996)
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Identification and analysis of the human and murine putative Genomics 34 (3), 328-333 (1996)
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Neuherberg, GERMANY  COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing consortium of the German Genome Project.  This clone (DKPZp451J114) is available at the RZPD in Berlin.  This clone (DKPZp451J114) is available at the RZPD in Berlin.  Please contact the RZDD Ressourcencentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/.  FEATURES  L. 4560  / Acqualifiers / Ab_xref="RZPD:DKFZp451J114" / Ab_xref="RZPD:DKFZp451J114" / Ab_xref="RZPD:DKFZp451J114" / Alone="DKFZp451J114" / Lissue type="human skeletal muscle" / Acome = "DKFZp451J14" / Lissue type="human skeletal muscle" / Acome = "DH10B; sites Not synonym: hlcc1). Vector pSportl; host DH10B; sites Not sage="adult" + Sal!"	Ouery Match 99.6%; Score 1095.2; DB 9; Length 4560; Best Local Similarity 99.7%; Pred. No. 1.4e-252; Matches 1097; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ATGCCGGGGGGTCCTGGGACCGGCGGTTACCTGCTCTACTACCTGCATGGGGGCC 60	61 TITIGGGBACCAGCCGATCATCTTGGGCTTCTCTGCAAAGCTGCTAAACCGT	OY 121 ACCTTGGCTGCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCTTTACCAACCTC 180	Oy 181 CATGIGICCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGCTATC 240	Oy 241 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCCTGACTGGCCCCCTGAGAGCGGGTG 300	Oy 301 GCATACTGCTTTGAGGTGGCAGCCCAGAAGCCCAGATAAGAAGACGTGCCCCATGAAG 360	OY 361 GAAGGAAACCCTTTGGCCATTCTGGGATCAGTTTCATGTGAGTTTCAAGAGTGGAG 420	Qy         421 CTTTTACAGGCATTCCTTCAGTGCTTCCTACAGAGAACATGGAGGCCAGAGATTTCT         480           Db         471 CTTTTACAGGCATTCCTTCAGTGCTTCCTACAGACACATGGAGCCAGAGATTTTCT         530           Qy         481 CCAAAGGAACTCCGTGCTTCCTCCAGGAGCCCAGTTCCCCGTCCTAGAA         540           Db         531 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGTTCCCCGTCCTAGAA         590           Qy         541 GAACACAGGCACTACAGAAGTACATGGTATGGTCAGACGAATGGTGAAGACGGAGAG         600           Qy         591 GAACACAGGCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGAGAG         600           Qy         601 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGAGAG         600           Qy         601 GACCAGAATCATGCCCCCTTTGTCCGCCCTTATGTGGGCATTTGGCTATGGCTTTCATTGGCCATTGGCTT         10           bb         651 GCCCAGATTCATGGCCCCTTTGTCCGGCCTTTATGTGGGCATTTGGCTCT         600           ccadaatTCATGCCCCCTTGTCCCGCCCTTATGTGGGCATTGGCTTTCATGGCCTT         710           cot         GGCCAGAATTCATGGCCCATTGTCGGCCCTTTGTCGCGCATTGGCTCT         710           cot         GGCCAGAATTCATGGCCCATTGTCCGGCCCTTATGTGGGCATTGGCTCTTCTGCGCATTGGCTCT         710           cot         GGCCAGAATTGGCCACCTTGTCCCGCCCTTTGTCCGCCCTTTCTTCTGCGCATTGGCTCT         710
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Martinez-Duncker,I., Mollicone,R., Candelier,J.J., Breton,C.
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fut12 gene; pofut1 gene; prote
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Pan troglodytes (chimpanzee)
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966 CCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGA 1025
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1 (bases 1 to 5009)
Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 4 25-DEC-2001;
GENEWYECH INC
OS Unidentified
PN JP 2001527389-A/4
PD 25-DEC-2001
PF 31-JAN-1997 US 08/792498,26-NOV-1
PF 31-JAN-1997 US 08/792498,26-NOV-1
PR 31-JAN-1997 US 08/792498,26-NOV-1
PF 31-JAN-1997 US 08/792498,26-NOV-1
PF ST CO-fucosyltransferase
CC Topology; Linear;
CC O-fucosyltransferase
CC Topology; Linear;
CC O-fucosyltransferase
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CAGTCGGTCTATGTTGCTACTGATTCCGAGGTTATGTGCCTGAGGCTCCAACAGCTCTTC 969
                                                   AAAGGGAAGGTGAAGGTGAGGCCTGAAGCCTGAGGTGGCCCAAGGTCGACCTGTACATC 960
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Sequence.8 from patent US 6270987.
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	GAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT 12
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ò	126 GGCTGTCCCTCCGTCGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCATGT 185
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ò	186 GTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATCAGCTT 245
අු	121 GTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATCAGCTT 180
à í	46 GGAGGATTCATGGAGAAGCTGGCACCCACCCACCCACCCCTGAGAAGCGGGGTGGCATA 30
<b>a</b>	BI GGAGGATTICATGGAGAAGCTGGCACCCACCCACTGGCCCCTGAGAAGCGGGTGGCATA 24
λ δ	306 CTGCTTTGAGGTGGCCAGCCAGCCAGATAAGAAACGTGCCCCATGAAGGAAG
ô	66 AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT 42
Db	9
ò	426 TACAGGGATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCTCCCAAA 485
QQ	361 TACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTCTCCCAAA 420
λŏ	486 GGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGTTCCCCGTCCTAGAAGAACA 545
Dp	421 GGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGTTCCCCGTCCTAGAGGAACA 480
Ολ	46 CAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGCGAGAGGCCCA 60
d d	481 CAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGAGGGGGAGAGGGCCCA 540
λ	606 GAITCAIGCCCACCITGTCCGGCCCTAIGIGGGCAITCATCTGCGCAITGGCTCTGACTG 665
Op	s41 dartcardcccaccriforccddcccriardidddcarrcacdddariddcrcrdacrd 600
ò	666 GAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCTCTCC 725
QQ Q	601 GAAGAACGCCTGTGCCAFGCTGAAGGACGGACTGCAGGCTCGCACTTCAFGGCCTCTCC 660
ò	6 GCAGTOTGTGGGCTA.CAGCCGCACAGCGGCCCCCCTCACGATGACTATGTGCCTGCC
QQ	
ò	786 TGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTC 845
Db	721 TGACCTGAAGGAGTCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTC 780
٥'n	846 GGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTGAAAGG 905
Dp	TACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCT
δ	906 GAAGGTGAAGGTGAGGCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGG 965
Op	841 GAAGGTGAAGGTGGTGAGCTTGAAGCTGGCCCAGGTCGACCTGTACATCCTCGG 900
δλ	966 CCAAGCCGACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGA 1025
DÞ	CAAGC

Search completed: November 9, 2005, 07:59:59 Job time: 4964.62 secs

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Adg6824 Novel can
Aak79915 Human imm
Aal03344 Human rep
Ach32225 Human end
Ach3532 Human end
Abl13947 Drosophil
Abl13946 Drosophil
Abl13852 Drosophil
Abl13852 Drosophil
Abl44539 Human spl
Abr44539 Human spl
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Aak52494 Human pol
Aav65634 First Eco
Aad07629 Human sec
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Adf81754 Leukaemia
                                                                                                                                         8, 2005, 23:23:13; Search time 642.158 Seconds (without alignments) 10140.369 Million cell updates/sec
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Aav65633 Plasmid c
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                                                                                                                                                                                                                                         US-09-774-954-16
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1 ATGCCCGCGGGCTCCTGGGA......CTGCGGGACGAGTTCTGATT 1100
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       4390206 segs, 2959870667 residues
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                                                                                             OM nucleic - nucleic search, using sw model
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ABN44539
AAZ98210
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Ada71938 Rice dene		Aca31561 Prokaryot	Aad08215 Human gen	Aah97782 Murine 7-	Adg80232 Brain-spe	Adq84111 Human tum	Adb75488 Prostate	Aav65637 Primer am	Aav65635 Northern	Ada69815 Rice gene	Aca43606 Prokaryot	Abd01472 Pseudomon	Abd01484 Pseudomon	Abx46567 Bovine ES	Adi62782 Human apo	Ade77025 Human cDN	Ade25660 Human cDN	Ach26305 Human adu	Abt10150 Human bre	Aca64963 Human cor	Ads63598 Bacterial	Ads63974 Bacterial	Adt41577 Bacterial	Aah52044 Mycobacte
ADA71938	ADA71938	ACA31561	AAD08215	AAH97782	ADQ80232	ADQ84111	ADB75488	AAV65637	AAV65635	ADA69815	ACA43606	ABD01472	ABD01484	ABX46567	ADI62782	ADE77025	ADE25660	ACH26305	ABT10150	ACA64963	ADS63598	ADS63974	ADT41577	AAH52044
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5.	4.2	3.9	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.4	3.4	3.4	3.4
٦. 0	46.2	42.4	41.2	40.6	40.4	40.4	40.4	40	40	40	39	39	39	38.6	38.6	38.6	38.6	38.4	38.4	38.4	37.8	37.8	37.8	37.8
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## ALIGNMENTS

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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                           O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                                                                                             Location/Qualifiers
1. .1100
/*tag= b
/note= "this actively expressed O-fucosyltransferase agenence is claimed for in claim 9"
                                                                                                                                                                                                                       heart O-fucosyltransferase"
                                                                        Human heart O-fucosyltransferase encoding DNA.
                                                                                                                                                                                                            /*tag= a
/product= "human
          AAV65632 standard; DNA; 1514 BP.
                                                                                                                                                                                                                                                                                    97WO-US023401
                                                                                                                                                                                                                                                                                                        97US-00792498.
                                                   16-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                           Spellman MW;
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P-PSDB; AAW80571.
                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                    17-DEC-1997;
                                                                                                                                                                                                                                                                                                       31-JAN-1997;
26-NOV-1997;
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                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                               06-AUG-1998
                               AAV65632;
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CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCCTTCACTGCCTTTGTGAAG 1020
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                                                                                                                                                                                                                                                                                                                                                                                     960
                                                                                                                                                                                 This represents the nucleotide sequence of the plasmid construct used for the expression of human heart O-fucosyltransferase. The human O-fucosyltransferase and although an epidermal growth factor (BGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of
CTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epidermal growth factor diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4140. .5333
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4218. .4235
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O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                              CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
                                                                                                                                                          AAAGGGAAGGTGAAGGTGGTGAGCCTGAGGTGGCCCCAGGTCGACCTGTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid construct for expression of human O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human O-fucosyl:transferase able to glycosylate domains - useful for diagnosis and treatment of overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4218. .4235
/*tag= b
/note= "polyhistidine tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCGGGACGAGTTCTGATT 1100
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P-PSDB; AAW80573.
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Synthetic.
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26-NOV-1997;
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     781
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                                                                     This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EPP) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. diagnosis and treatment of conditions associated with overexpression of o-fucosyltransferase, to probe associated with overexpression of Pucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EPF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
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                                                                                                             Sequence 11284 BP; 2947 A; 2602 C; 2624 G; 3111 T; 0 U; 0 Other;
O-fucosyltransferase, e.g. mutants with increased affinity for
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                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target (TAT) cDNA DNA326813, SEQ ID NO:5725
                 AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC
                                                                CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG
AAAGGGAAGGTGAAGGTGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC
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                                                                                                 CGGGAGCGGGACCTCCAGGGGGGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCTAAG
                                                                                                                          5256 CGGGAGCGGGACCTCCAGGGGAGGCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 5725; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; cytostatic; gene; ss.
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptide acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acids and antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonistes, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with

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Best Local Similarity
Matches 1097; Conserv
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(KERN/) KERN W.
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increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lug cancer, bladder cancer, particularly cancer, bladder cancer, particularly cancer, carvical cancer, carvical cancer, carvical cancer, carvical central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC
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                                                                                                                                                                                           DB 13; Length 5218;
                                                                                                                                                       Sequence 5218 BP; 1255 A; 1274 C; 1334 G; 1355 T; 0 U; 0 Other;
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99.7%; Score 1096.8; DB 13; Lengt
Best Local Similarity 99.8%; Pred. No. 2.7e-305;
Matches 1098; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a patient sample.
                                                                                                                                                                                                                        CGGGAGCGGGACCTCCAQGGAGCCGTCTTTTTTTTCTTCGGCATGGACAGGCCCCTAAG
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                                 CTCGGCCAAGCCGACCTTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG
                                                                                                              AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTCGACCTGTACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kohlmann A, Schnittger S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukaemia-related DNA sequence #2310.
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(UYLU-) UNY LÜDWIG MAXIMILIANS.
(HAFE/) HAFERLACH T.
(SCHO/) SCHOCH C.
                                                                                                                                                                                                                                                                                                                                          CTGCGGGACGAGTTCTGATT 1100
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Eils R, Brors B, Mergenthaler S;
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Matches 1048; Conserv
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Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to oytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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R, Wang
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Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
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27-APR-2000; 2000US-00560875.
20-UJN-2000; 2000US-00590075.
19-UJL-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
AAK51510 standard; cDNA; 5230
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(first entry)

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Human, cytokine; cell proliferation, cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomedulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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AAK52494 standard; cDNA; 4850

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolesis regulating activity, tissue growth factor activity, immunoadulatory activity and activity tissue growth factor activity, immunoadulatory activity and activity tissue growth factor activity, immunoadulatory activity and activity to cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM8002) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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94.7%; Score 1041.4; DB 4; Length 4950;
Best Local Similarity 99.4%; Pred. No. 2.5e-289;
Matches 1045; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
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Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                          03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UNJ-2000; 2000US-00598075.
19-UJJ-2000; 2000US-00538075.
11-SEP-2000; 2000US-0065436.
15-SEP-2000; 2000US-00653561.
20-CT-2000; 2000US-0063361.
30-NOV-2000; 2000US-0063325.
                                                                                                                                                                                              05-FEB-2001; 2001WO-US004098
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Homo sapiens
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O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;

Homo sapiens

97US-00792498 97US-00978741

(GETH ) GENENTECH INC.

Spellman MW 1998-437477/37.

Υ,

Wang

P-PSDB; AAW80577

97WO-US023401

17-DEC-1997; 31-JAN-1997; 26-NOV-1997;

06-AUG-1998

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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving

overexpression of the enzyme

also 300 ŏ 185 120 245 180 305 240 365 425 485 This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial cDNA encodes for a protein of unknown function from myeblast celline KG-1. The invention provides a human heart Ofucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-9 GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCTGAGAAGCGGGTGGCATA 1 GAACCAGGCGGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT GGCTGTCCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCATGT GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTGGCATA TACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCTCCCAAA 66 GAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT GGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCATGT GTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATCAGCTT GTCCTACCAGAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATCAGCTT AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT 301 AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT TACAGGCATTTCCTTCAGTGCTTCCTACAGAGACAATGGGAGCCAGAGATTTTCTCCAAA Gaps Score 1033.4; DB 2; Length 5009; Pred. No. 5.1e-287; 0; Mismatches 1; Indels 0; Sequence 5009 BP; 1235 A; 1195 C; 1268 G; 1311 T; 0 U; 0 Other; Example 1; Fig 11; 90pp; English 93.9%; Query Match Best Local Similarity 99.9 Matches 1034; Conservative fucosyltransferase 126 61 186 121 246 181 306 366 426 셤 장 : 염 원 셤 g ò ò g ð ò à ð

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O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; nucleotide fragment of human KIAA0180.

BP.

AAV65634 standard; cDNA; 5009

RESULT

AAV65634
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616 CACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTGGAGAAGAAGCCC 675
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21-JUL-2000; 2000US-0219666P.
                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; AAE03110.
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                                                                                                                                                                  Human, secreted protein, proliferative disorder, cancer, tumour, foetal abnormality, developmental abnormality, haematopoietic disorder; fietal abnormality, developmental abnormality; haematopoietic disorder; imfamment system disorder; ALDS, autoimmune disease, rheumatoid arthritis; inflammation, allergy, neurological disorder, Alzheimer's disease, Parkinson's disease, cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepais; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastroinestinal disorder; programcy-related disorder; gene endocrine disorder; infection; wound healing; vulnerary, cell culture; chemotaxis; food additive; binding partner identification; chromosome 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein-encoding gene 18 cDNA clone HMWEY26, SEQ ID NO:69
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/product= "Human secreted protein precursor"
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protein genes, and AAE03052-AAE03156 represent the proteins they encode.

AAE03127-AAE03150 represent human secreted protein fragments. The genes

AAE03127-AAE03150 represent human secreted protein fragments. The genes

and their corresponding secreted proteins are useful for preventing,
treating or ameliotating medical conditions, e.g., by protein or gene

therapy. Pathological conditions can be diagnosed by determining the

conditions in the new genes. Specific uses are described for each of the

mutations in the new genes. Specific uses are described for each of the

conditions and include developing products for the diagnosis or treatment of

mutations in the new genes. Specific uses are described for each of the

conditions and include developing products for the diagnosis or treatment of

proliferative disorders, cancer, tumours, focetal and developmental

conditions and include developing products for the diagnosis or treatment of

phornalities, haematopoletic disorders, diseases of the immune system,

AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

callergies, neurological disorders, felicophrenia, asthma, skin disorders

disorders, pregnancy-related disorders, endocrine disorders, and

disorders, pregnancy-related disorders, endocrine disorders, and

infections. The proceins can also be used to alw wound healing and

confinition partners, and in chemotaxis, and can be used as a food

confinition partners, and in chemotaxis, and can be used as a food

additive or preservative to modiffy storage properties of printing

confining partners, and in chemotaxis, and can be used in alleviating

symptoms associated with the disorders mentioned above, and in diagnostic

immunosassy e.g., radioimmunosassy or enzyme linked immunoscopent assay

(ELISA). The present sequence represents a human secreted protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
/transl_except= (pos:4. .6, aa:Xaa)
/transl_except= (pos:0. .12, aa:Xaa)
/transl_except= (pos:13. .15, aa:Xaa)
/transl_except= (pos:142. .444, aa:Xaa)
/note= "Xaa equals any of the naturally occurring L-amino
acids; CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels 0;
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43.0%; Score 473.4; DB 4; Length 915;
Best Local Similarity 98.4%; Pred. No. 8.7e-126;
Matches 477; Conservative 1; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 915 BP; 209 A; 253 C; 247 G; 202 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                 1...3
/*tag= b
4...495
/*tag= c
/*troguet= "Mature human secreted protein"
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1; SEQ ID NO 8126; 41pp; English.

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TGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCTCTCCGCAGTGTGTG
                                                                                   GAGATCCAGAGGGCTGTGAAGCTCTGGGTGGGTCGCTGGATGCCCCAGTCGGTCTACGTT
                                                                                                                                                 GCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAG
                                                                                                                                                                                                        GCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAG
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                                                                                                                                                                                                                                                                                                       CACTITATIGGGAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGAGCGGAACCTC
                                                                                                                                                                                                                                                                                                                               CAGGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGAGTTC
                                                                                                                                                                                                                                                                                                                                                       436 CAGGGGAGSCCGTCTTCTTTCGGCATGGACAGGCCCCCTAAGCTGCGGGACGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               canine microarray; drug screening; toxicity assay;
environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         canine microarray-related DNA sequence SeqID8126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC. (PFIZ ) PFIZER PROD INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-561890/54.
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine mucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as disagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that conducing electronic Northerns that allow the user to determine the cell producing electronic Northerns that allow the user to determine the cell producing electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expression level of a given gene in a particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The ethicod that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver (likelihood that a compound or test agent will induce various specific disease, protein adduct formation or hepatitis), those of the kidney, hard the toxins. The methods are also useful for predicting or elucidating compound or test agent will not predicting or elucidating compound or test agent will not be expression profile compound or test agent due to the similarity of the expression profile induced by a known toxin. The present sequence is the compound or test agent due to the similarity of the expression profile induced by a known coxin. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCAATCTCCATGTGTNCTACCAGAAGTACTTCAAGCTNNAGCCCCTCNAGGNNTACCA
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Pred. No. 1.8e-106;
0; Mismatches 54; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 610 BP; 155 A; 171 C; 149 G; 129 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production of a canine microarray of the invention
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89.0%;
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Matches 446; Conservative
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12. SEP-2000; 2000US-0231958P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-02324997P.
14-SEP-2000; 2000US-0234234P.
15-SEP-2000; 2000US-024424P.
16-SEP-2000; 2000US-024424P.
16-SEP-2000; 2000US-024424P.
16-SEP-2000; 2000US-024424P.
16-SEP-2000; 2000US-024424P.
17-NOV-2000; 2000US-024623P.
17-NOV-2000; 2000US-024623P.
17-NOV-2000; 2000US-024623P.
17-NOV-2000; 2000US-024623P.
17-NOV-2000; 2000US-024623P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2
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2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34727
                RESULT 10
AAK79915
XX
XX
AAK79915
XX
XX
AAK79915;
XX
YOUNOW-2001 (first entry)
XX
Human; immune/haematopoietic antigen
XX
XX
Human; immune/haematopoietic immu
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Homo sapiens.
XX
XX
Homo sapiens.
XX
XX
Homo sapiens.
XX
XX
Homo sapiens.
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XX
AAK72000;
XX
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AAK72000;
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AAK72000;
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AAK72000;
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AAK72000;
AAK7
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 6032
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20000S-0225214P
20000S-022526FP
20000S-022526P
20000S-022526P
20000S-022520P
20000S-022570P
20000S-022570P
20000S-022570P
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2000US-0214886P.
2000US-0215135P.
2000US-0216647P.
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2000US-0220963P.
2000US-0220964P.
2000US-0224518P.
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2000US-0226681P.
2000US-0226868P.
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2000US-0227009P.
2000US-0228924P.
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                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                  WO200155320-A2
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                     21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
               AAL03344;
               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
c ancers and cancer metastesses of haematopoietic-derived cells. AAK64703
c o AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK849492 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2600 TGTGCCTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGG 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFGCCCAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGC 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 GCTCTGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 34727; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-025130P.

05-DEC-2000; 2000US-025198P.

05-DEC-2000; 2000US-025198P.

06-DEC-2000; 2000US-0251479P.

08-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-025198P.

08-DEC-2000; 2000US-025198P.

08-DEC-2000; 2000US-025199P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483426/52
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Best Local Similarity
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AAL03344
ID AAL03
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2000US-0232400P

14-SEP-2000;

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PR 14-SEP-2000; 2000US-0232064P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0233064P.
PR 22-SEP-2000; 2000US-023499P.
PR 25-SEP-2000; 2000US-023499P.
PR 25-CCT-2000; 2000US-023499P.
PR 25-CCT-2000; 2000US-023499P.
PR 25-CCT-2000; 2000US-024198P.
PR 26-CCT-2000; 2000US-024198P.
PR 26-CCT-2000; 2000US-024198P.
PR 26-CCT-2000; 2000US-024198P.
PR 26-CCT-2000; 2000US-0244617P.
PR 26-NOV-2000; 2000US-024617P.
PR 27-NOV-2000; 2000US-024617P.
PR 27-NOV-2000; 2000US-024917P.
PR 27-NOV-2000; 2000US-024
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                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      656 GCTCTGACTGGAAGGACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGTCGCACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2480 GCTCTCCGTAGAAGAACGCCTGTGCCTTGCTGAAGGACGGGACTCGCAGCTTCA
                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.8%; Score 251.2; DB 4; Length 10331; Best Local Similarity 97.0%; Pred. No. 3.4e-61; Matches 256; Conservative 0; Mismatches 8; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                 Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 6032; 1297pp + Sequence Listing; English.
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                                                                                                                                          Rosen CA, Barash SC, Ruben SM
08-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251989P.

11-DEC-2000; 2000US-025199P.

05-JAN-2001; 2001US-025499P.
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                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide comprising any one of 3843 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypetide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide conformation also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGTGTCTCCTCCTTCACTGCCTTTGTGAAGCGGGAGCGCGGACCTCCAGGGGAGCCCG 1047
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                                                                                                                                                       New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868 GAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAGGTGAAGGTGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            928 AAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 AAGCCTGAGGTGGCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGC
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                                                                                                        Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 233; DB 9; Length 479; 100.0%; Pred. No. 1.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 479 BP; 99 A; 140 C; 143 G; 97 T; 0 U; 0 Other;
                                                                                                       Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
                                                                                                                                                                                                                        Claim 1; SEQ ID NO 19437; 44pp; English.
                                                                                                       Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACH35532 standard; cDNA; 477 BP
30-JUL-2001; 2001US-00918995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233; Conservative
                                                    STACHE-CRAIN B.
                                                                                                       Labat I,
                                                                                                                                                                                               antisense DNA or RNA.
                          DRMANAC R T.
                                                               DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 233; Conserva
                                                                                                                              WPI; 2003-615964/58
                                      LABAT
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                                     (LABA/)
(STAC/)
(DICK/)
(JONE/)
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The invention relates to an isolated polynuclectide comprising any one of 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynuclectide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/RST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPFO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
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Matches 237; Conservative
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(STAC/) STACHE-CRAIN
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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RESULT 14

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Human endothelial cell cDNA #3665.

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.034 ATCCTTACCTGGACTTGGCCATTCTCGGACAGTCGAACCTTTTATCGGCAACTGTATA 1093
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ID ABL13946 standard; cDNA; 3264 BP.
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                                                                                                                                                                                                                                                                                                    Drosophila, developmental biology, cell signalling, insecticide,
pharmaceutical, gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

15.1%; Score 166.4; DB 4; Length 12

Best Local Similarity 51.5%; Pred. No. 376-37;

Matches 563; Conservative 0; Mismatches 466; Indels

Matches 563; Conservative 0; Mismatches 466; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 36323; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                      ABL13947 standard; cDNA; 1209 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                       26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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ABL13947

ABL13947

AND
ABL139
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completed: November
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1864 TCGGAGCGAGTGTCATTTGCTACAAGGAACGATATAGCCTTCAGCAGGAGAAGAACGAT 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1744 Tritcacaragacrirgergegericagaerrerargegeceacrircarrirgargrecarcar 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1684 AGCAACGAGGCTGCCAAGTGGCAGACCAAATATCCTGCAGAATCATATCCCGTACTCGCG 1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 GAGAAGCGGGTGGCATACTGCTTTGAGG-----TGGCAGCCAGCGAAGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGATAAGAAGACGTGCCCCATGAAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCATGTGAGTTTCAACAAGTCGGAGCTTTTTACAGGCATTTCCTTCAGTGCTTCCTAC 453
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 TGCATGGGGCGCTTTGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 TTCACCAACCTCCATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTAC
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                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 36320; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3264 BP; 904 A; 742 C; 758 G; 860 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
13.7%; Score 150.4; DB 4; Length 3
Best Local Similarity 50.9%; Pred. No. 2.4e-32;
Matches 541; Conservative 0; Mismatches 476; Indels
                                                                                                                                                                                Myers EW;
                                                                                                                                                                                Li PWD,
                                                                                         23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                    23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                              Venter JC, Adams M,
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                                                                                                                                             CORP NY.
                                                                                                                                                                                                                                P-PSDB; ABB69843
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                  27-SEP-2001
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ATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGGCCCAGATTCATGCCCACCTTGTC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1444 CACGTCAAGGATAGCCAGCATCTGTTTGCCTCGCCGCAGTGCTTGGGCTATAAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 ATGCTGAAGGACGG-----GACTGCAGGCTCGCACTTCATGGCCTCTCCGCAGTGT
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BP459416 AUI37536 35525 MA UI-E-EJO-UI-E-CLI-

BP457865 AU117392 UI-M-HN0-601487689

CN348922 BP459416 BR0137536 BG894786 BR714731 BR714731 BR711732 CN4159072 CN4159072 CN25952 BE878197 CV22952 BE878197 CV23953 BR5165030 BR516539 BR516539 BR516539

601900828 601150556 602578756

7968 Full

Mus muscu

AGENCOURT AGENCOURT BY728337 BB642654

CF239348 BY728337

OM nucleic

Run on:

Sequence:

Searched:

Database

Result

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 9100 GENY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nRNA linear HTC 21-JUL-2004 of T cells (Jurkat cell line)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR617950.1
HTC; CNSLT_CDNA.
HTC; CNSLT_CDNA.
HOmo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1555)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGCCCGCGGGCTCCTGGGACCCGGCCGTTACCTGCTCTACTGCCCCTGCATGGGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1096.8; DB 3; Length
Pred. No. 5e-291;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="T cells (Jurkat cell line)
10-normalized"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR617950 1555 bp mRNA full-length cDNA clone CS0DJ008YF12 of T c Cot 10-normalized of Homo sapiens (human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ008YF12"
                                                    BP459416
AU137356
BC894786
BM714731
BM714731
BM714731
CW597786
AU17392
CW59789
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99.8%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.8
Matches 1098; Conservative
 Faraday Avenue
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(c) 1993 - 2005 Compugen Ltd.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eli, W.B., Gruber; C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30371746.

Contact: Ganoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.ons.fr, Web: www.genoscope.ons.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                  BX353274 linear EST 08-APR-2004
BX353274 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC003Y311 5-PRIME, mRNA sequence.
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/moi Lype="mcNA"
/db Arzef="Lexon.9606"
/clone="CS0DC003YJ11"
/fissue type="NEUROBIASTOWA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBIASTOWA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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        24.1 AGCTTGGAGGATTTCATGGAGACTGGCACCCACCCACCCCTGAGAAGCGGGGG
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        34.9 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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ATGCCTGCGGGCTCCTGGGACCCGGCTGGTTACCTGCTCTACTGCCCTGCATGGGGCGC 168
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The Farmary Consolution and the Kirch Genome Exploitation Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Adachi, "Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Harozane, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakatu, J., Saltoh, K., Sakai, K., Sakazume, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Sakai, K., Sakazume, N., Sano, H., Saaki, C., Sakazume, N., Sano, H., Saaki, C., Sakazume, N., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Likeda, Y., Tagami, M., Tagawa, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Likeda, Y., Shibata, K., Shinagawa, A., Shiraki, The Institute of Physical and Chemical Research Group, RIKEN Genome Exploration Research Group, Kanagawa, 230-0464, Japan (E-mail:genome-rese@gencriken.jp, URL:http://genome.gencriken.jp, Tal:al-45-503-9216)

Fax:81-45-503-9216

CDNA library was preparated and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Drivision of Experimental Animal Research in Riken contributed to Driverson of Encyclopedia Project and Genome Science Laboratory in Riken Driverson and Encyclopedia Project of Genome Encyclopedia Project of Genome Encyclopedia Project of Genome Exploration Research in Riken Contributed to Driverson and Encyclopedia Project of Genome Exploration Research in Riken Contributed to Driverson and Encyclopedia Project of Genome Sciences Center and Genome Sciences Center and Genome Sciences Center and Genome Scien
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/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_Etage="10 days neonate"
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Please visit our web site for further details
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/db_xref="taxon:10090"
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Location/Qualifiers
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/strain="C57BL/6J"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                      CCAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTTCCTKAGCTCCAACAGCTCTT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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	AKO44629 AKO44629 LOCUS DEFINITION Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A330028F21 product:protein O-fucosyltransferase 1, full ACCESSION AKO44629. WRESION AKO44629. WRESION AKO44629.	_	REFERENCE 2 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., ILOh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159	REFERENCE 3 RICHALA, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., AUTHORS Shibata, K., Itoh, M., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Itegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Orawa, K., Tanaka, T., Matsuura, S., Nawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. TITLE RIKEN integrated sequence analysis (RISA) system-184-format sequencing oideline with 384 multicabillary sequencer	JOURNAL Genome Res. 10 (11), 1757-1771 (2000) MEDLINE 20530913 PUBMED 11076861 REFERENCE 4 AUTHORS THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM CONSortium. TITLE Functional annotation of a full-length mouse cDNA collection Depressive Research Group (2001)		Hori,F., Imotani,K., Ishii,Y., Itoh,W., Kagawa,I., Kasukawa,T., Katoh,H., Kwawi,U., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakai,K., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Taqami,M., Tagawa,A., Takahahi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
Query Match         80.5%;         Score 885.4;         DB 3;         Length 3611;           Best Local Similarity         88.0%;         Pred. No. 1.3e-222;           Matches 964;         Conservative         0;         Mismatches 131;         Indels 0;         Gaps 0;           Qy         5 CGGGGGCTCCTGGACCGGGCGGTTACCTGACTGACCCGCATGGGGGCTTTG 64         CGGGGGCTCCTGGACCGGGTTACCTGCTACTACTGCCTGC	65 GGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACGTACCT	185   TGTCTTACCAAATACTTCAAACTTGAGGCCCTCTACCATCGGGTTGTGTGTG	365 GAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGGTTT		1	TIGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	905 1001 965 1061 1063

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AGENCOURT 6611915 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5431669
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIER), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 23-0-0045, Japan (E-mail:genome-res@gsc.riken.jp, WBL:http://genome.gsc.riken.jp, Tel:81-45-503-9222, Pax:81-45-503-9222,
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CMGRFGWQADHFLGSLARAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQ
AYHRVVSLEDFWENLAPSHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQF
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                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of Reurbialology, Harvard Medical School, 220 Longwood Ave., Boston, Ma Veurobiology, Harvard Medical School, 220 Longwood Ave., Boston, Ma URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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O-fucosyltransferase 1 (MGD|MGI:2153207, GB|NM_080463,
evidence: BLASTN, 99%, match=1290)
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db_xref="taxon:10090"
/clone="A930028F21"
/tissue_type="retina"
/clone_lib="RIKEN full-length enr/dev_stage="adult"
34. .1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 884.2; DB 3;
Pred. No. 2.6e-232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /proteIn_id="BAC32009.1"
/db_xref="GI:26336653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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964; Conservative
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on May 5, 2003 this sequence version replaced gi:30377055.
Contact: Genoscope
Contact: Genoscope
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.ons.fr, Web: www.genoscope.ons.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMXSpORT overce. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX345989
BX345989 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED HOmo sapiens CODJO08YF12 5-PRIME, mRNA sequence.
BX345989
                                                                                                                                                                                                                                                                                                    GIACATCCTCGGCCAAGCCGACCTTT-ATTGGCAACTGTGTCTCCTCCTTCACTG--- 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGGTT 897
                                                                                                                                                                                                                                                                                                                                                     912 GTAAATTCTTCGGCAAGCCGAACCCTTTAATTGGGAACTGTGGCCCCCCTCCTTCCCGGGC 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                             792 GCCCAGTCGGTCTACGTTACTGATTCCGAGAGTTATGTGCCTGAAGCTCCACAGCTC
                                                                                                                                                                                             898 TTCAAA--GGGAAGGTGAAGGTGGTG--AGCCTGAAGCCTGAGGTGGCCCAGGTCGACCT
                                                                                                                                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAJ008DC06QP1&c=9980.f. Location/Qualifiers
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Pred. No. 1.1e-186;
1; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                            1010 CCTTTGTGAAGCGGGAGCGGGACCTCCAGGGGAGGCCGTCTTT 1055
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ilarity 99.5%;
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Homo sapiens
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/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_98"
/note="DTATE | Part | Part |
/note="DTATE | Part |
/note="DTATE | Part |
/note="DTATE |
/note="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 GAGCTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGACAATGGAGCCAGAGATTT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 GAGGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGC 657
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                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can letond through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1904 row: e column: 14
High quality sequence stop: 629.
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llarity 93.0%; Pred. No. 1.3e-193;
Conservative 0; Mismatches 54;
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5431669"
   Fissue Procurement: ATCC
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German Genome Project.

No s1 sequence available.
This clore (DKF2P76200115) is available at the RZPD in FPlease contact the RZPD: Ressourcenzentrum, Heubnerweg i Please contact the RZPD: Ressourcenzentrum, Heubnerweg i Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        719;
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/note="Vector: pSport1; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                     Score 717.4; DB 1;
Pred. No. 1.9e-186;
); Mismatches 1;
                                                                                                                                                                                                (MeWo
                                                                                                       1. 719
/ organism="Hono sapiens"
/ organism="Hono sapiens"
/ db xref="texon:9606"
/ clone="DKF2p76200115"
/ tissue_trype="melanoma (Mev stage="adult"
/ lab_host="DH10B"
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1 (Dases 1 to 719)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S. EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Contact: MIPS
MIPS
MIPS
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Conter (DKEZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                       AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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                     TTTGGGAACCAGCCGATCACTTCTTGGGCTCTCTGGGCATTTGCAAAGCTGCTAAACCGT
                                                                      ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC
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DKFZp76200115_5', mRNA sequence.
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/ Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="1566"
// Clone="CSODM014YK11"
// Clone="CSODM014YK11"
// Clone lib="Homo sapiens FETAL LIVER"
// Clone lib="Homo sapiens FETAL LIVER"
// Clone lib="Homo sapiens FETAL LIVER"
// Organ: liver; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primeT. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCWVSPORT 6 vector. Library was not normalized."
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2 rue Gaston Cremieux, CP 5706 - 91057 EVX cedex - FRANCE
Email: sequencepe.cns.fr. Neb: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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      361 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420
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11, (bases 1 to 898)
11, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31030014.
                                                                                                                  CTTTTTACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT
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This sequence belongs to sequence cluster 9980.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0AM014AF06QP1&c=9980.f.
Location/Qualifiers
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//organism="Homo sapiens"
//organism="mxxx"
//db_xref="taxon:9606"
//clone="Ixxxon:9606"
//clone="Ixxon:9606"
//clone="Ixxon:9606"
//clone="Organ: pooled lung and spleen; Vector: pcWV-SPORT6;
//clone=lib="NVH" OrG 122"
//clone=lib="NVH" OrG 122"
//clone=lib="NVH" OrG 122"
//clone=lib="NVH" OrG 122"
//clone=lib="NVH" Site 2: BcoRV (destroyed; RNA source spleen, and 20-22 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (BroxV site is destroyed upon cloning). Average insert size is destroyed upon cloning. Average insert size and was constructed by C. Gruber [Invitrogen]. Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                 BUKANYOKEA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; BUKANYOKEA; Metazoa; Chordata; Craniata; Perimetes; Catarrhini; Hominidae; Homo.

E. 1. (bases 1 to 889)

S. NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Inditional institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llnl.gov

Place: Libralis sequence stop: 880.

Locatian/Qualifiers

Locatian/Qualifiers
BI524031 889 bp mRNA linear EST 29-AUG-2001
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                                                                                                                                                                    Homo sapiens (human)
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Best Local Similarity 99.1
Matches 758; Conservative
                                                         mRNA sequence.
BI524031
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    and Magness, C.L.
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cDNA_Library
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Sequenced on 2004.07.21. 611 Q20 bases. Library Preparation:
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Bioschences Inc. For further information, see
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                                                                             2203 Airport Way S, Suite 450, Seattle, WA 98134,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                        /Bex="male"
/lab host="Electromax DH10B"
/clone lib="Katze MNLV"
/note="Organ: liver; Vector: pDONR 222;
Site_2: BsrG I; Created from CloneMiner
Construction kit (catalog #18249-029)"
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.2%; Score 673.2; DB 7; Best Local Similarity 94.1%; Pred. No. 3.3e-174; Matches 743; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                            /organism="Macaca nemestrina"
/mol type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                 FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
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Plate: CL000531 row: E column: 09
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POLYA=NO.
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/clone="IBIUW:29960"
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                                                                                                                                                                                      http://www.macaque.org
PCR PRimers
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Macaca nemestrina
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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              Score 706.6; DB 5;
Pred. No. 2e-183;
4; Mismatches 10;
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            cch 64.2%;
al Similarity 97.8%;
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1 ATGCCGGGGGCTCCTGGGACCGGGCTGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60	TITGGGAACCAGGCGATCACTICTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT	142 TTTGGGAACCAGGCCGATCACFTCTTGGGCTCTCTGGCATTTGCAAAGCTCCTAAACCGT 201 121 ACCTTGGCTTCCTTGGATTACAATTGCAATCCTCTTGTGTTGTCTCTT 180	202 ACCTIGGETIGTCCTCCTTGTATTGTATTGTATTGTATTGTATTGTAT		241 AGCTIGGAGGATITCATGGAGAAGCTGGCACCCACCCACCCGCCGGGAGCGGGTG 300	301 GCATACTGCTTTGAGGTGGCAGCCCAGGAAGCCCGGATAAGAAGACGTGCCCCATGAAG 360 	361 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG 420 	421 CTITITACAGGCATTICCTICAGIGCTICCTACAGAGACAATGGAGCCAGAGATTITCT 480	481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCTCCCCGTCCTAGAA 540 	541 GAACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGAC-GGGAGA 599 	600 GGCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGGCTTTGGCTC 659	660 TGACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGACTGCAGGCTCGCACTTCATGGC 719 	720 CTCTCCG 726         802 CTCTCCG 808	2 BP144264 ON BP144264 full-length enriched swine cDNA library, adult ovary Sus	GCOTA CLORE OVRU10034GU9 5', MKNA BEQUENCE.  BP144264.1 GI:40393735 EST. crofa (pig)	SM SGYOLD ME GAZOG; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Suidae; Sus. B 1 (bases 1 to 801) S 1 (bases 1 to 801)	Okumura, N. Hamasima, N. and Awata, T. PEDS (Fig BST Date Explorer): construction of a database derived from porcine full-length cDNA libraries Nucleic Acids Res. 32 (1), D484-D488 (2004) Animal Genome Laboratory, Genome Research Department Animal Genome Laboratory, Genome Research Department
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Db 575 CCAAAGGAACATCCGGTGCTTGCCCTGCCGGGAGCCCCGGCCCAGTTCCCTGTCCTGGAA 634  Qy 541 GAACACAGGCCACTACAGAAGTACATGGTCAGACGAAATGGTGAAATGGTGAAAGACGGAAAG 600	635 GAACACACCACTGCAAAAGTACATGGTATTGTTCAGACAATGGTAAGGACAGAAAA	b 695 GCCCAGATATATCCCGCCCTGTT-CCGGCCCTATGTGGGGGTTCATCGCGGTTCGGCTT 658	OY 659 CTGACTGGAAAGACGCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGG 718  Dh 755 CTGACTGGAAAATGCTGTGCTATGTTATGTATGTATGTAT	719 CTCTCCCCGTGTGTGTGCCCCTTTCTTTTTTTTTTTTT	GGGGGCCTAACGCCCCCCCCCCCCCCCCCCCCCCCCCCC	Db 875 GTGCCTGCCT 884	RESULT 11 BG747760 BG747760 BG747760 BET BG747760 BET BG747760 BET BG747760 BET BG747760 BET BG747760 BET BG77760 BET BG777760 BET BG777760 BG777760 BG7777760 BG7777760 BG7777760	ION N DS	_	REFERENCE I (bases 1 to 808) AUTHORS NIH-MGC thtp://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)		by: The I.M.A.G.E. Consortin rcyte Genomics, Inc. 4GC clone distribution infor A.G.E. Consortium/LLNL at:	ntp://mage.lin.gov Plate: LiCMM675 row: n column: 14 High quality sequence stop: 808. FEATURES COURTED 1 Coation/Qualifiers		I, Site 2: ionally ing 5'	adaptor: GsCACAGAG(G). Library constructed by ling hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Skratagene) and Superscript II RT (Life Technologies).	ORIGIN  Query Match 60.2%; Score 662.2; DB 4; Length 808; Best Local Similarity 95.3%; Pred. No. 3 4e-171; Matches 693; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

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AGENCOURT 10055799 NIH MGC_134 Mus musculus CDNA clone
IMAGE:6509783 5', mRNA_sequence.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 134"
/note="Vector: pCWV-SPORT6.1; Site 1: EcoRV; Site 2: Not1;
/note="Vector: pCWV-sport6"
/ Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by Resden, Invitrogen Corp. Note: this is a NIH_MGC Library."
                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe.remail.nih.gov.
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14077 row: j column: 24
High quality Sequence Stop: 702.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 988)
                                         TCGCCACGGACTCTGAGAGTTACCTGCCGGAGATCCAGCAGCTCTTCAAAGGAAAGGTGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Mus musculus"
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/clone="IMAGE:6509783"
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National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan.
Tel: +81-29-838-8627
Fax: +81-29-838-867
Fax: +81-29-88
Fax: 
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/tissue_type="0vary"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult ovary"
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iive 0; Mismatches 88;
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E i (bases 1 to 874)

NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Umpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

NR Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl..gov
Plate: LLAMMISOO row: j column: 23
High quality sequence stop: 798.
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BI757540 G1:15749118
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TGTGTCCTACCAAAAGTACTTCAAACTGGAGCCTCTCCAAGCCTACCATCGGGTTGTCAG 387
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                                        CCTGGAGGACTTCATGGAAAATCTGGCACCCTCCCACTGGCCCCCTGAGAAGCGAGTGGC
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Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Courcement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11290 row: o column: 13
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                                                  B1410783 947 bp mRNA linear EST 14-AUG-2001
602963556F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119332 5',
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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larity 86.9%; Pred. No. 1.6e-162;
Conservative 0; Mismatches 107; Indels 8;
                                                                                                                                                                                                                     Mus musculus (house mouse)
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482 903 362 429 422 489 549 541 550 AAAAGAGCATCCTGTGCTCGCACTGCCTGGGGCCCCGGCACAGTTCCCTGTCCCTGGAGG 609 601 699 661 721 788 781 846 AAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGGTTCCCCGT-CCTAGAAG TTTTACAGGCATTTCCTTCAGTGCTTCCTACAGGAGCAATGGAGCCAGAGATTTTCTCC 490 GTTCACAGGCATTTCCTTCAGCGCCTCCTACAAAGAACAATGGACCCAGAGATTTCCTGC 610 AACACAGGGAGCTCCAGAAGTACATGGTGTCAGATGAGATGAGATGATGAGGACGGGAAGA 729 ACTGGAAGAATGCCTGTGCCATGCTGAAGGATGGAACTGCAGGCTCACACTTCATGGCTT ATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCCAGATAAGAAGACGTGCCCCATGAAGGA AGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCT 430 AGGAAATCCTTTTGGGCCATTCTGGGACCAGTTTCATGTGAGTTTCAATAAGTCAGAACT AACACAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAAATGGTGAAGACGGGAAGAG CCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGGCATTCATCTGCGCATTGGCTCTG CTCCGCAGTGTGTGGGCTACAGCGCAGCACACAGCGGCCCCCCTCACGATGACTATGTGCC TGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCC **ACTGGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCT** 879 AATCGGTCTACATCGC-ACAGACTCTGAGAGCTACGTG 940 842 AGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTG 9, 2005, 10:38:07

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Sequence 4752, Ap Sequence 9986, Ap Sequence 6032, Ap Sequence 1211, Ap Sequence 1211, Ap Sequence 18160, A Sequence 18160, A Sequence 18082, A Sequence 17287, A Sequence 114097, Sequence 312, Appl Sequence 312, Appl Sequence 114097, Sequence 112, Appl Sequence 112, Appl Sequence 112, Appl Sequence 113, Appl Sequence 114, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 1171, Appl

us-09-774-954-16.rnpb

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Run on:

Sequence:

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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
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Publication No. US20040241645A1
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 7
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION - «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
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COMPUTER READABLE FORM:
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2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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(c) 1993 - 2005 Compugen Ltd.
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CORRESPONDERS ESE Genettecu.

STREET: 1 DNA WAY

CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: MIRM FOR COMPATIBLE
APPLICATION DATA:
REPLICATION NUMBER: US/08/978,741
FILING DATE: 30-MATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
MARE: SVODOGA, CTAIG G
REGISTRATION NUMBER: 99,044
REFERENCE/POCKET NUMBER: 99,044
REFERENCE/POCKET NUMBER: 99,044
REFERENCE/POCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATIO
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US-09-774-954-1
US-09-774-954
; Sequence 1, Application US/09774954
; Publication No. US20040241645A1
; Publication No. Tang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Pucosyltransferase
NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
: CORRESPONDENCE Geneticch, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
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181 CATGTGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATGGGTCATC
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                                                                          NAME: Svoboda, Craig G.
REGIGFRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 191041P1
TELECOMUNICATION INFORMATION:
TELEPAX: 650/225-1489
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1100; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-774-954-16
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De 1081 CTGCGGGACGACTICTGATT 1100  BESSILT 3  US-09-744-954-4  1 MADICAL IN	Db 256 ACTTGGCTGCCTTGGATTGGATGCAGCTCACAGCCTCCTTTCACCACCTC 315  Qy 181 CATGTGTCCTACCAGAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC 240  Db 316 CATGTGTCCTACCAGAAGTACTTCAGGTGGGCCCTCCAGGCTTACCATCGGGTCATC 375  Qy 241 AGCTTGGAGATTTCATGGAGAAGCTGGCCCCACCACCAGGCTTACCATCGGGTG 300  Db 376 AGCTTGGAGATTTCATGGAGAAGCTGGCCCCCACCAGGCCCTGAGAAGCGGGTG 300  376 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCACCACCCCCTGAGAAGCGGGTG 300
ATTRECCOCCOCCCTCTCCTCCCCCCCTTTTTCCTCTCTCTCTC	CTGGGCGAGCGACCACTTATTGGCAGCGGCCCCTTCACTGGCGAGCGA

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99.9%; Score 1098.4; DB 11; Length 11284;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 0; Mismatches 1; Indels 0; G
                                                                   disk
COMPUTER READABLE FORM:

WEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM FO Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURENT APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
TLING DATE: 30-Jan-2001
PRIOR APPLICATION NUMBER: US/08/978,741
FILING DATE: 36-NOV-1997
APPLICATION NUMBER: US/08/978,741
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SYODGA, CARAGG R
RGGISTRATION NUMBER: 39,04
REPERENCE/DOCKET NUMBER: 91
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 93,04
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 92,04
REPERENCE/DOCKET NUMBER: 93,04
REPERENCE/DOCKET NUMBER: 91,041P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOURCE: 11284 base pairs
TYPE: Nucleic Acid
STRANDEDISSS: Single
TYPE: Nucleic Acid
STRANDEDISSS: Single
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TOPOLOGY: Linear seq ID NO: 5:
US-09-774-954-5
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                                                                                                                                                                                                                                                 CITITIACAGGCAITICCTICAGTGCTICCTACAGAGAACAATGGAGCCAGAGAITITCT 615
                                                                                                                                                                                                                                                                                                                                  735
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                                                                     CTITITACAGGCATITCCTICAGIGCTICCTACAGAGAACAAIGGAGCCAGAGAITTTCT 480
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Sequence 5, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
ITLLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
CTIY: South San Francisco
STREET: Call South San Francisco
STREET: GOUNTRY: USA
COUNTRY: USA
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Query Match         99.7%;         Score 1096:8;         DB 16;         Length 5218;           Best Local Similarity 99.8%;         Pred. No. 0;         2;         Indels 0;         Gaps 0;           Matches 1098;         Conservative 0;         Mismatches 2;         Indels 0;         Gaps 0;           Oy 1 ArgcccgcgGCTCCTGGGACCCGGCTGCTTACTGCCTCTACTGCCCTGCATGGGGCG 60         Db 119 ArgCcTGCGGGCTCCTGGGACCCGGTTACTGCTCTTGCTCTTGCTCTTGCTCTTGCGGCTTACTGCGCTTACTGGGGCGC 178           Oy 61 THTGGGAACCAGGCCGATTCTTTGGGCTCTTTGGGCTTATTGCAAGCTGCTAAACCGT 120         Db 179 TTTGGGAACCAGACCGATCACTTCTTGGGCTTCTTGGGATTTGCAAAGCTGCTAAACCGT 238	CTCCTTTCACCAACCTC 18 CTCCTTTCACCAACCTC 29 CTTACCACGGGTCATC 24 CTTACCATCGGGTCATC 35 CTTACCATCGGGTCATC 35	CACTGGCCCCTGAGAAGCGGGTG 30  [	Qy         361 GAAGGAAACCCCTTTGGCCATTCTGGGATTTCATGTGAGTTTCAACAAGTCGGAG 420           Db         479 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACACGAG 538           Qy         421 CTTTTTACAGGCATTCTCTTCAGTGCTTCCTACAGAGAACGAAC	0
QY         601 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT         660           Db         4836 GCCCAGATTCATGCCGCCTATGTGGGCATTCATCTGCGCATTGGCTCT         4895           QY         661 GACTGGAAGAACGCCTGTGCCCATGGTGCAGACTGCAGCTTCATGGCTCT         4895           Db         4896 GACTGGAAGAACGCCTGTGCCATGCTGAAGACGGACTGCAGCTTCATGGCC         4955           QY         721 TCTCCGCAGTGTGGAGACGCCCCCCCACGATGACTATGTGC         780           Db         4956 TCTCCGCAGTGTGGGCTACAGCAGCACAGCACCCCCCTCACGATGACTATGTGC         780           Db         4956 TCTCCGCAGTGTGGGCTACAGCAGCACAGCACCCCCTCACGATGACTATGTGC         5015	QY         781 CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 840           Db         5016 CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC 5075           QY         841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCTACAGCTCTTC 900           Db         5076 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCTACAGCTCTTC 5135	QY         901 AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGACCTGTACATC 960           Db         5136 AAAGGGAAGGTGAAGCTGAGCCTGAAGCCTGAGGTCGACTGTACATC 5195           QY         961 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCATGCTTTGTGAAG 1020           Db         5196 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCATGCTTTGTGAAG 1020           Db         5196 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTCCTTCACTGCTTTGTGAAG 5255	Oy         1021 CGGAGCGGACCTCCAGGGAGGCCGTCTTCTTTCTTCGGCATGGACAGGCCCCCTAAG 1080           Db         5256 CGGGAGCGGACCTCCAGGGAGGCCGTCTTCTTCTGGCATGGACAGGCCCCCTAAG 5315           Qy         1081 CTGCGGACGACGACGACGATT 1100           Db         5316 CTGCGGACGACGACTTCTGTT 1335	RESULT 5  Sequence 168, Application US/10301822  Publication No. US2030148410A1  Sequence 168, Application US/10301822  Publication No. US2030148410A1  GENERAL INPORMATION:  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Millennium Pharmaceuticals, Inc.  APPLICANT: Ramatkar, Shubbargi  APPLICANT: Ramatkar, Shubbargi  APPLICANT: Monahan, John E.  APPLICANT: Thibodeau, Stephen N.  APPLICANT: Hurbarlor Burgart, Lawrence J.  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  TITLE OF INVENTION: THERAPY OF COLON CANCER  TITLE OF INVENTION: THERAPY OF COLON CANCER  TITLE OF INVENTION: THERAPY OF COLON CANCER  TITLE OF INVENTION: WIPPLER: US 60/319, 971  FILE REFERENCE: MPMOI-029PZRM  CURRENT APPLICATION NUMBER: US 60/381, 988  FRIOR FILING DATE: 2002-11-21  PRIOR FILING DATE: 2002-05-05  PRIOR FILING DATE: 2002-05-05  NUMBER OF SEQ ID NOS: 228  SOFTWARE: Fasts of or Windows Version 4.0  SEQ ID NO 168  LENGTH: 5218  TYPE: DNA  ORGANISM: HOMO Sapiens  PRATURE:  NAMAEKEY: COS  NAMAEKEY: CO

09   00.0   00	Oy 721  Db 839  Qy 781  Db 899  Qy 841  Db 959  Qy 901  Db 1019	Oy 1021 CGGGGGGGCCCCCTAGGGGGGGCCGTCTTCTTCGGCATGGACGCCCCTAAG  Db 1139 CGGGAGCGGGACCTCCAGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAG  Oy 1081 CTGCGGGACTCTGATT 1100  Db 1199 CTGCGGGACGAGTTCTGATT 1218	NESULT 7  105-074-74-954-7  105-09-774-954-7  106-08-774-954-7  107-08-10-704-0241645A1  107-08-10-10-10-10-10-10-10-10-10-10-10-10-10-
1021   CGGGAGCGGCCTCCAGGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAG   1080	RESULT 6  10S-10-56-157-4752  10S-10-56-157-4752  10S-10-56-157-4752  10S-10S-10S-10S-10S-10S-10S-10S-10S-10S-	Ouery Match  Query Match  Best Local Similarity 99.7%; Score 1096.8; DB 22; Length 5218;  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1098; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 1098; Conservative 0; Mismatches 2; Mismatches 0; Mismatches 2; Mismatches 0; Mismatches 2; Mismatches 0; Mismatches 2; Mismatc	61 TITIGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 120  179 TITIGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 238  121 ACCTTGGCTGCTCCTCTTGGATTGAGTACCAGCATTTGCAAAGCTGCTAACCGT 238  122 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCTCCTTTCACCAACCTC 298  123 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCTCCTTTCACCAACCTC 298  126 CATGTGTCCTACCAGAAGTACTTCAAGCTGGATCACAAGCTCCTTTCACCAACCTC 298  127 ACCTTGGAGGATTTCATGGAGAAGCTGGACCCCCCAGGGCTTACCATCGGGTCATC 358  128 AGCTTGGAGGATTTCATGGAGAAGCTGGCCCCCCCTGAGAGAGCGGGTC 310  129 GATACTGGTTCCTACAGAAGAAGCTGGCACCCCACCCAGGGCTTACCATGGAGAGCGGGTG 310  140 GCATACTGGTTTGAGGAAGAAGCTGGCACCCCACTGAGAGAGCGGGTG 310  151 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCCACTGAGAGAGCGGGTG 310  152 AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGAGAGAGA

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RESULT 9
US-10-956-157-4751
; Sequence 4751, Application US/10956157
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Best Local Similarity 99.8
Matches 472; Conservative
                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo
US-10-956-157-9986
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                                                                                       Query Match 93.9%; Score 1033.4; DB 11; Length 5009; Best Local Similarity 99.9%; Pred. No. 4.1e-314; Matches 1034; Conservative 0; Mismatches 1; Indels 0;
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        SEQUENCE CHARACTERISTICS:
LENGTH: 5009 base pairs
LENGTH: 5009 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID IUS-09-774-954-7
  ID NO: 7:
INFORMATION FOR SEQ
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APPLICANT: Wyeth

TITLE OF INVENTION: UNDERLY AND HUMAN PROTEASES

FILE REFERENCE: 2004-10-04

CURRENT APPLICATION: WHOREN: USDO (AM 101081)

TITLE OF INVENTION: WHOREN: USJO (AM 101081)

TITLE OF INVENTION: WHOREN: USJO (AM 101081)

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION WHOREN: USJO (AM 101081)

CURRENT APPLICATION WHOREN: USJO (AM 101081)

CURRENT APPLICATION WHOREN: USJO (AM 101081)

SOFTWARE: PATENT OF INVENTION: USBO (AM 101081)

SOFTWARE: PATENT OF INVENTION: USBO (AM 101081)

SOFTWARE: PATENT OF INVENTION: USBO (AM 101081)
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GCGGGACCTCCAGGGGAGGCCGTCTTCTTCGGCATGGACAGGCCCCCTAAGCTGCG
                                                                                                   GCGGGACCTCCAGGGGAGGCCGTCTTCTTTCTTCGGCATGGACAGGCCCCCTAAGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTTGGCTGTCCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 GCATACTGCTTTGAGGTGGCAGCCCAGCGAAGCCCAGATAAGAAGAAGACGTGCCCCATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC
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Pred. No. 1.9e-137;
0; Mismatches 1;
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2599
                                                                                                                                                                                                                                                                               2600 TGTGCCTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGG 2659
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                                                                                                                                                                                                 2480 GCTCTCCGTAGAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCA
                                                                                                                                                                       TGGCCTCTCCGCAGTGTGTGGGCTACAGCCGCAGCAGCGGCCCCCCTCACGATGACTA
                                                                                                                                                                                                                                                          TGTGCCTGCCTGACCTGAAGGAGATCCAGAGGCTGTGAAGCTCTGGGTGAGGTCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868 GAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGGTGAAGGTGGTGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            928 AAGCCTGAGGTGGCCCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCACTTTATTGGC
                                                                                       656 GCTCTGACTGGAAGAAGGCCTGTGCCATGCTGAAGGACGGGACTGCAGGTCGCACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 TCTTCTTTCTTCGCCATGGACAGGCCCCCTAAGCTGCGGACGAGTTCTGATT 1100
       Length 10331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.2%; Score 233; DB 10; Length 479; Best Local Similarity 100.0%; Pred. No. 1.7e-62; Matches 233; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-18-995-19437
i Sequence 19437, Application US/09918995
j Publication No. US2030073623A1
i GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE PERFENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,995
NUMBER OF SEQ ID NOS: 38054
i SOFTWARE: PERFENCE: 1999-01-20
i NUMBER OF SEQ ID NOS: 38054
i SEQ ID NO 19437
LENGTH: 479
    Score 251.2; DB 10; Length
Pred. No. 9.4e-68;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2720 TCTTCAAAGGGAAGGTATGTGTGG 2743
                                                                                                                                                                                                                                                                                                                                                                                                                             896 TCTTCAAAGGGAAGGTGAAGGTGG 919
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US-09-318-995-22744
US-09-318-995-22744
Februarication No. US20030073623A1
FUBLICATION No. US20030073623A1
FEBRAL INFORMATION:
PAPLICANT: Hyseq, Inc.
         22.8%;
Local Similarity 97.0%;
Les 256; Conservative 0
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ORGANISM: Homo sapiens
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           Query Match
Best Local S
Matches 256
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: WILLIAM
TITLE OF INVENTION: HUMAN OSTEOARTHAITIS AND HUMAN PROTEASES
FILE REFERENCE: 03.1896-04.3000 (AM 10.081)
CURRENT PELLING DATE: 10.04/10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEP UD NO 4751
LENGTH: 1506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TITGGGAACCAGGCCGATCACTICTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCCCCCCCCCCCCCCCCCCCCCCCCCCCCTCCTACTGCCCCCTCCATGGGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6032, Application US/09764891
| Sequence 6032, Application US/09764891
| Publication No. US20030077808A1
| GENERAL INPORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVERTION: Nucleic Acids, Proteins, and Antibodies |
| TITLE OF INVERTION: Nucleic Acids, Proteins, and Antibodies |
| CURRENT APPLICATION NUMBER: US/09/764,891 |
| CURRENT FILING DATE: 2001-01-17 |
| Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 10231 |
| SEQ ID NO 6032 |
| LENGTH: 10331 |
                                                                                                                                                                                                                                                                                                                                                                  Length 1506;
                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                             Score 471.4; DB 22;
Pred. No. 1.9e-137;
0; Mismatches 1; I
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Best Local Similarity 99.8%;
Matches 472; Conservative
                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4751
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; ORGANISM: Homo sapiens
US-09-764-891-6032
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US-09-764-891-6032
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ATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACGGTACCTTGGCTGTCCCTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGGGTGGAGT----ATCGTAGGGTGAACTGCGATCCCGTCAGGTACCGTTCAACA
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                                                                                                                                                                                                                                                                       GGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGCTTTGGGAACCAGGCCG
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                                                                                                                                                                                                                                45;
                                                                                                                                                                                     Length 1209
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                   DB 26;
                                                                                                                                                                                 15.1%; Score 166.4; DB 26;
51.5%; Pred. No. 2.4e-41;
tive 0; Mismatches 486;
      NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 18161
LENGTH: 1209
                                                                                                                                                                              Query Match
Best Local Similarity 51.5'
Matches 563; Conservative
                                                                                             TYPE: DNA ORGANISM: DROSOPHILA
                                                                                                                        ; ORGANISM: DROSO
US-11-097-143-18161
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Pred. No. 5.9e-59;
0; Mismatches 8; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACID
EXPRESSION OF 10,000
      OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFPLICANT: VERICE: J. CTAIG
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC.
TITLE OF INVENTION: DRARAYS, FOR DETECTING EXPITITLE OF INVENTION: DRASOFHILA GENES.
TITLE OF INVENTION: DRASOFHILA GENES.
FILE REFERENCE: CLOOD'28
FILE REFERENCE: CLOOD'28
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 06/15,832
PRIOR APPLICATION NUMBER: 60/161,931
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/161,769
PRIOR FILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
PRIOR PRIOR DATE: 1999-12-29
PRIOR PRIOR DATE: 1999-12-29
PRIOR PRIOR DATE: 1999-12-28
PRIOR PILING DATE: 1999-12-28
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PRIOR PRIOR DATE: 1999-12-28
PRIOR PRIOR DATE: 1999-12-28
PRIOR PRIOR DATE: 1999-12-29
PRIOR PRIOR DATE: 1999-12-29
                               CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILIANG DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 477
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Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NR APPLICATION NUMBER: 60/175,693
RR FILING DATE: 2000-01-12
NR APPLICATION NUMBER: 60/184,831
RR FILING DATE: 2000-02-24
RR APPLICATION NUMBER: 60/191,637
RR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n = A,T,C or G
US-09-918-995-22744
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.2%;
Best Local Similarity 96.3%;
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(477)
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                                                                        AAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTCGGTCTAC 852
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Sequence 11501, Application US/09783590
Patent No. US20020110850A1
Patent No. US20020110850A1
APPLICANT: Dillon, Patrick J.
APPLICANT: Braseltine, William A.
APPLICANT: Rosen, Craid A.
APPLICANT: Rosen, Craid A.
APPLICANT: Rosen, Craid A.
APPLICANT: REPERRENCE: Pole C. 2CI
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 0200-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                    CGG---CCCTATGTGGGCATTCATCTGCGCATTGGCTCTGACTGGAAGAACGCCTGTGCC
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    289 GAGAAGCGGGTGGCATACTGCTTTGAGG-
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US-09-783-590-11501
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US-11-097-143-18160/C

| Sequence 18160, Application US/11097143
| Publication No. US2005020858A1
| GENERAL INFORMATION:
| APPLICANT: Venter, J. Craig
| APPLICANT: et al. J. Craig
| TITLE OF INVENTION: BENECTION KIT, SUCH AS NUCLEIC ACID
| TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE
| FILE REFERENCE: CLOOG/28
| FILE REFERENCE: CLOOG/28
| FRIOR APPLICATION NUMBER: 60/15,191
| PRIOR APPLICATION NUMBER: 60/161,932
| PRIOR PILING DATE: 1999-10-19
| PRIOR PILING DATE: 1999-110-19
| PRIOR PILING DATE: 1999-110-19
| PRIOR PILING DATE: 1999-110-19
| PRIOR PILING DATE: 1999-110-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR PILING DATE: 2000-03-23
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR PILING DATE: 2000-03-23
| PRIOR APPLICATION NUMBER: 60/175,693
| PRIOR PILING DATE: 2000-03-23
| NUMBER OF SEQ ID NOS: 43008
| SOSTWWARE: FASSED FOR WINDOW VERSION 4.0
| LENGTH 4.354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1984 creccentric central contrata contrata contrata de la crecce de la contrata del contrata de la contrata de la contrata del contrata de la contrata del contrata de la contrata del contrata de la contrata del contrata del contrata de la contrata de la contrata del contrata del contrata de la contrata de la contrata del contr
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                                                                                                                                                                                                                                                                                                                                                    1094 cererracerdedarredaaaaaadddaacdadarerecacerrrecaredracerer 1153
                                                                                                                                                                                          1034 ATCCTTACCTGGACTTGGCCATTCTCGGACAGTCGAACCACTTTATCGGCAACTGTATAT 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 TCCATGGGGCGCTTTGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 CTGCTAAACCGTACCTTGGCTGTCCCTCTTGGATTGAGTACCAGCATCACAAGCCTCCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCGGGTCATCAGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCCT 288
                                                                                                                     --- CCCAGGTCGACCTGTACATCCTCGGCCAAGCCGACCATTTATTGGCAACTGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.7%; Score 150.4; DB 26; Length 3264; Best Local Similarity 50.9%; Pred. No. 3.7e-36; Matches 541; Conservative 0; Mismatches 476; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     1058 TCGGCATGGACAGG 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OKGANISM: DRUSO)
US-11-097-143-18160
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178 CICCATGIGICCTACCAGAAGTACTICAAGCIGGAGCCCCTCCAGGCTTACCATGGGTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 ATCAGCTT-GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCT---GAGAA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 GCGGGTGGCATACTGCTTTGA--GGTCGCAGCCCAGCGAAGCCCAGAT-----AAGAAGA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 GGGGTGGCATAATGCTTTTNAGGTGGCGAGCCCAGCGANGCCCAGATTAAGNAAGGACG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 Arcadcrirggadgarrircargaaaagcragcacccaccacragacccurraagaagc 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.4%; Score 114.6; DB 9; Length 402;
Best Local Similarity 83.9%; Pred. No. 3.4e-25;
Matches 177; Conservative 0; Mismatches 23; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 CGTGCCCCATGAAGGAAGGAAACCCCTTTGG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 INGACCCCATGAAGGAAGGAAACCCTTTTG 371
                                                                                                                                                                         TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (9)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (27)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (30)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (333)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (334)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (342)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (342)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (386)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (386)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (490)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (490)
OTHER INFORMATION: n equals a,t,g, or c
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11501
LENGTH: 402
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Search completed: November 9, 2005, 15:51:17 Job time : 988.698 secs

(OFREI) NIMALIS EDAY ZIHT

Sequence 11943, A Sequence 12011, A Sequence 11977, A Sequence 13025, A Sequence 13025, Batent No. 5386025 Patent No. 5386025

Sequence 1, Sequence 1 Sequence 191, Sequence 221,

Sequence

Sequence 1

Sequence Sequence

OM nucleic

Run on:

Sequence:

Searched:

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ATGCCCGCGGGGCTCCTGGGACCCGGCTTACCTGCTCTACTGCCCCTGCATGGGGGCGC
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US-09-410-551B-1
US-09-940-316B-1
US-09-252-991A-11943
US-09-252-991A-11947
US-09-252-991A-11977
US-09-949-016-13025
US-07-91B-023-1
5386025-5
US-08-314-083B-1
US-08-314-083B-1
US-08-314-595-1
US-08-316-557A-3
US-08-316-557A-3
US-08-316-557A-3
US-08-316-257A-3
US-08-316-257A-3
US-08-234-258-1
US-10-237-551-221
US-09-294-298A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Generical) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/792498 FILING DATE: 39.044 REGISTRATION NUMBER: 39.044 REGISTRATION NUMBER: 39.044 REFERENCE/DOCKET NUMBER: 19041P1 TELECOMPUNICATION INPERMITION: CONTOUR COMPANION: CONTOUR CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
CITY: South San Francisco STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALI GNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-978-741-16
; Sequence 16, Application US/08978741
Patent No. 6100076
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 1100, Conservative
                                                                                              102053
102053
1843
1843
5962
5975
5975
5975
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STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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36.8
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Sequence 1225, Ap
                                                                                                                                                                   9, 2005, 02:15:54; Search time 199.044 Seconds (without alignments) 9042.764 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1100
1 ATGCCCGCGGGCTCCTGGGA.......CTGCGGGACGAGTTCTGATT 1100
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2 6/ptodata/1/ina/5A COMB.seq:*
/cgn2 6/ptodata/1/ina/5B COMB.seq:*
/cgn2 6/ptodata/1/ina/6A COMB.seq:*
/cgn2 6/ptodata/1/ina/6B COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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-09-270-767-30507
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US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-978-741-10
-08-978-741-12
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                                                                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents NA:*
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Maximum DB seq length: 200000000
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Sequence 16, Application US/0933729A
Setent No. 6270987
GENERAL INFORMATION
PAPLICANT: Mang. Vang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
TITLE OF INVENTION: O-Fucosyltransferase
CURRENT APPLICATION UNDRES: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
SEQ ID NO: 21
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ORGANISM: Homo Sapien
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Db 721 TCTCCGCAGTGTGGGCTACAGCCGCACAGCGGCCCCCTCACGATGACTATGTGC 780	OY 781 CTGCCTGACCTGAAGGGATCCAGAGGCTGTGAAGCTCTGGGTGGCTGGC	Qy 841 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC 900	Qy         901         AAAGGGAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGGCCCAGGTCGACCTGTACATC         960           Ph         1	961 CTCGGCCAAGCCGACCATTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTG	Db 961 CTCGGCCAAGCCGACCTTTATTGGCAACTGTGTCTCCTTCACTGCTTTGTGAAG 1020 Oy 1021 CGGGAGCGGGAACTTCAGGGGAGGCGTCTTTTTTTTGGGAGAGGCCCCTAAG 1080	1021 CGGGAGCGGGACTCCAGGGAGGCCGTCTTCTTCTTCGGCATGGACAGGCCCCTAAG	Qy         1081         CTGCGGGACGAGTTCTGATT         1100           Db         1081         CTGCGGGACGAGTTCTGATT         1100	PRSIII.7 3	US-08-978-741-1 ; Sequence 1, Application US/08978741 ; Patent No. 6100076	; GENERAL INFORMATION: ; APPLICANT: Yang Wang, Michael W. Spellman ; TITLE OF INVENTION: O-Fucosyltransferase ; NUMBER OF SEQUENCES: 17	CARRESPONDENCE ADDRESS:  STREET: 1 DAW Way	ညီ	COUNTKY: USA  ZIP: 94080  COMPTER READABLE FORM:  MENTIFF WYDE. 2 F. 104 M. Flores: 3101	Gert Ger	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/978,741 ; FILING DATE: 26-No. 6100076-1997 ; CLASSIFICATION: 435	; FRICK AFFLICATION DATA: ; PILING DATE: 31 ; ATTORNEY/AGENT INFORMATION:	) NAME: SVODGGA, CTAIG G. ; REGISTRATION NUMBER: 39,044 ; REFRENCE/DOCKET NUMBER: P1041P1 ; TELECOMMUNICATION INFORMATION:	; TELEPAN: 650/225-1489 ; INPORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS:	; TENOTH: 1514 base pairs ; TYPR: Nucleic Acid ; STRANDEDNESS: Single ; TOPOLOGY: Linear	US-08-978-741-1 Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    GACTGGAAGAACGCCTGTGCCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genencech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVORDOM, CTASJ G.
REFERENCE/DOCKET NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PD041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-1489
TELEPHONE: 650/25-1489
TELEPHONE: 650/25-1489
TELEPHONE: GSO/592-980
TELEPHONE: GSO/592-980
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TELEPHONE: GSO/592-980
TELEPHONE: GSO/25-1489
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US-078-741-4
| Sequence 4, Application US/08978741
| Patent No. 6100076
| GENERAL INFORMATION:
| TITLE OF INVENTION: O-FUCOSYLTRANSFERSE
| TORRESPONDENCE ADDRESS:
| ADDRESSES: Genentech, Inc.
| STREET: 1 DNA WAY
| CITY: South San Francisco
| CONTRY: California
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TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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                                                                                                                                                                                                   APPLICANT: Wang Yang
APPLICANT: Wang Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Procosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
SEQ ID NOS: 21
; Sequence 2, Application US/0933729A; Patent No. 6270987; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
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US-09-333-729A-2
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Pred. No. 0;
0; Mismatches
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APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REPRENCE: P1041P1D1-Subscitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT APPLICATION NUMBER: US 08/798,741
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1300
                                                                          CTGCGGGACGAGTTCTGATT 1100
                                                                                                                                            ; Sequence 6, Application US/0933729A
; Patent No. 6270987
; GENERAL INFORMATION:
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US-09-333-729A-6
                                                                                            CTGCGGGACGAGTTCTGATT
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Best Local Similarity 99.9%;
Matches 1099; Conservative C
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                              Score 1098.4;
Pred. No. 0;
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Best Local Similarity
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        AGCTTGGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTG
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tive 0; Mismatches
; INFORMATION FOR SEQ 1D NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 11284 base pairs; STRANDEDNESS: Single; TYPE: Mucleic Acid TYPE: TOPOLOGY: Linear US-08-978-741-5
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Matches 1099; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 126-NO. 6100076-1997
CLASSIFFICATION NUMBER: 08/792498
FILING DATE: 31
FILING DATE: 31
FILING DATE: 31
FILING DATE: 31
FILING DATE: 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08978741
Patent No. 610076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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STREET: 1 DNA Way
STREY: South San Francisco
STATE: California
COUNTRY: USA
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5136 AAGGGAAGGTGAAGGTGAAGGCTGAAGCCTGAAGGCCCAGGTCGACCTGTACATC 5195	ò	246 GGAGGATTTCATGGAGAGGTGGCACCCACTGGCCCCCTGAGAAGCGGGTGCCATA 305
CTCGGCCAAGCCGACCATTTATTGGCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 102	qa	GGAGGATTTCATGGAGAAGCTGGCACCCACCCACTGGCCCCCTGAGAAGCGGGTGGCATA 24
5196 CTCGGCCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTTCCATTGCTGTGTGTAG 5255 1021 ÇGGGAGCGGGACCTCCAGGGGAGGCGTCTTTTTTTTTGGATGGA	රු සි	306 CTGCTTTGAGGTGGCAGCCGAGGAAGCCCAGATAAGAAGAGGTGCCCCATGAAGAAGG 365
	à	AAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTT
1081 CTGCGGGACGAGTTCTGATT 1100 	g &	AAACCCTTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAGCTTTTT TACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCTCCCAA
RESULT 8 US-08-978-741-7 ; Sequence 7, Application US/08978741	g &	TACAGGCATTTCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCTCCAAA GGAAAATCCGGTGCTTGCCTGCCAGGAGCCCCAGCCCAG
Patent No. 6100076 GENERAL INFORMATION: APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17	90 60 90	421 GGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGGTTCCCCGTCCTAGAGGAACA 480 546 CAGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGGCCCA 605
CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco	& a	GATTCATGCCCACCTTGTCCGGCCCTATGTGGGCCATTCATCTCGCGCATTGGCTCTGACTG           HILLHILLHILLHILLHILLHILLHILLHILLHILLHIL
	ζ Q	666 GAAGAACGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCCTCTCC 725 [
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC Comparible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)	ζζ O	GCAGTGTGTGGGCTACAGCCGCAGCAGCAGCCCCCCTCACGATGACTATGTGCCTGCC
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435	oy da	186   TGACCTGAAGGAGTCCAGAGGCTGTGAAGCTCTGAGTGAG
PRIOR APPLICATION DATA: - APPLICATION NUMBER: 08/792498 - FILING DATE: 31 - ATTORNEY/AGENT INFORMATION:	Qy Pp	846 GGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGG 905
NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1041P1 TELECOMMUNICATION INFORMATION:	Q QI	906 GAAGGTGAAGGTGAGCCTGAAGCCTGAGGTGGCCCAGGTGACCTGTACATCCTCGG 965
TELEPHONE: 650/225-1489 TELEPAX: 650/952-981 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:	& A	966 CCAAGCCGACCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGA 1025
MonGTH: 5009 Dase pairs TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear	ζ q	1026 GCGGGACCTCCAGGGGGGCCGTCTTCTTCTCGGCATGGACAGGCCCCCTAAGCTGCG 1085
Novery Match 93.9%; Score 1033.4; DB 3; Length 5009; Best Local Similarity 99.9%; Pred. No. 8.3e-302; Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0; '	λ <sub>O</sub> qa	1086 GGACGAGTTCTGATT 1100 
66 GAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTT 125 	RESULT US-09-3	RESULT 9 US-09-333-729A-8 ; Sequence 8, Application US/09333729A
126 GGCTGTCCCTCCGTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCATGT 185	; Paten ; Genera ; APPI ; APPI ; TITI ; FILE	atent No. 6270887  **BENEAL INFORMATION:  **APPLICANT: Spellman, wichael W.  **APPLICANT: Spellman, wichael W.  **TITLE OF INVENTION: O-Fucosyltransferase  FILE REFERENCE: Pl041PlD1-Substitute  **CURRENT APPLICATION NUMBER: US/09/333,729A

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15.3%; Score 168; DB 4; Length 1320;
Best Local Similarity 51.6%; Pred. No. 2.9e-40;
Matches 564; Conservative 0; Mismatches 485; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Drosophila melanogaster
US-09-270-767-14353
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GTCCTACCAAAGTACTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGTCATCAGCTT

GTCCTACCAAAGTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGGTCATCAGCTT

GTCCTACCAAAGTTCAAGCTGGAGCCCTCCAGGCTTACCATCGGGGTCATCAGCTT
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                                                                                                                                 Length 5009;
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                                                                                                                               DB 3;
                                                                                                                            Query Match 93.9%; Score 1033.4; DB 3
Best Local Similarity 99.9%; Pred. No. 8.3e-302;
Matches 1034; Conservative 0; Mismatches 1;
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 8
                                                                                          Homo Sapien
                                                                  5009
                                                                                             ; ORGANISM: HON
US-09-333-729A-8
                                                               LENGTH: 50
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFUTANTE: Patentin Ver. 2.0
SEQ ID NO 13022
LENGTH: 2034
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28905
                                                                                                                                                                                                                                                                                      CTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGGAAGG---TGAAGG
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Pred. No. 3.2e-07;
0; Mismatches 64
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; Sequence 28905, Application US/09270767
; Patent No. 6703491
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Patent No. 6703491

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30507
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Gaps

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837

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; LENGTH: 19228
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16285
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US-09-949-016-12127/C

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

SEGUENCE INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEABE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-3

SPRIOR FILING DATE: 2000-10-3

SOFTWARE FRANCE (CLOOS)

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FRANCE (CLOOS)

LENGTH 19227
                                                                                                           .
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                                                                                                                                                                                     971 CCGACCACTTTATTGGCAACTGTGTCTCCTTCACTGCCTTTGTGAAGCGGGAAGCGGG 1030
                                                                                                                                                                                                              1872 CGAACCACTTTATCGGCAACTGTATATCCTCTTACTCGGCATTCGTAAAAAGGGAACGAG 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGCCCGCGGGCTCCTGGGACCCGGCCGGTTACTGCTTACTGCCCTGCATGGG 56
                                   Query Match 5.3%; Score 58.6; DB 4; Length 2034; Best Local Similarity 60.2%; Pred. No. 4.8e-07; Matches 97; Conservative 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.1%; Score 56; DB 4; Length 19227; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 56; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                1031 ACCICCAGGGGAGGCCGICTICTTTCTTCGGCATGGACAGG 1071
                                                                                                                                                                                                                                                                                                     1812 Argrackackarrrrckarkarkarrakkarrakkarrakkar 1772
US-09-270-767-13022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , TYPE: DNA
; ORGANISM: Human
US-09-949-016-12127
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| CRGANISM: Human
| US-09-949-016-16285 | US-09-949-016-16285 | US-09-949-016-16285 | US-09-949-016-16285 | US-09-949-016-16285 | US-09-949-016-16285 | US-09-949-016-18285 | US-08-18285 | US-08-1828
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